```
gct gtc aca gct ata gtc cca gct gca gca atc att cgt gca cgt atg   1363
Ala Val Thr Ala Ile Val Pro Ala Ala Ala Ile Ile Arg Ala Arg Met
                410                 415                 420

cga gct tcc aag act ttc aac tat caa gac ttg ggt ccc ttg tcc gga   1411
Arg Ala Ser Lys Thr Phe Asn Tyr Gln Asp Leu Gly Pro Leu Ser Gly
            425                 430                 435

tgg aac aag tgg gtc att cgt tcg atc cca ctc aaa cga gct gaa tcg   1459
Trp Asn Lys Trp Val Ile Arg Ser Ile Pro Leu Lys Arg Ala Glu Ser
        440                 445                 450

atc aca gtc tcc cac ggt ggc ttc aga aaa gaa ctc cca gtt cga cgc   1507
Ile Thr Val Ser His Gly Gly Phe Arg Lys Glu Leu Pro Val Arg Arg
    455                 460                 465

aaa gtt gat gtt caa tgg att act gag gat ctc acg atc gag aat ctt   1555
Lys Val Asp Val Gln Trp Ile Thr Glu Asp Leu Thr Ile Glu Asn Leu
470                 475                 480                 485

caa ggt ctc gat cat gag ccc gtt ttc cac acg agt ccc cgc atc gaa   1603
Gln Gly Leu Asp His Glu Pro Val Phe His Thr Ser Pro Arg Ile Glu
                490                 495                 500

ttc ccc acc tct gga tca aac tgg gta att cag tat tca cag att ctt   1651
Phe Pro Thr Ser Gly Ser Asn Trp Val Ile Gln Tyr Ser Gln Ile Leu
            505                 510                 515

cca gat ggc agc ctc atc gaa atg gaa gat tac cca gtc gaa cct gaa   1699
Pro Asp Gly Ser Leu Ile Glu Met Glu Asp Tyr Pro Val Glu Pro Glu
        520                 525                 530

aac ttc gga tac gaa cta gac ctc ttc gaa gaa tcc gac gac cct tgg   1747
Asn Phe Gly Tyr Glu Leu Asp Leu Phe Glu Glu Ser Asp Asp Pro Trp
    535                 540                 545

gtc ggg caa ttt tta gta act ctg ctc aag gat gaa aaa gtc tat gaa   1795
Val Gly Gln Phe Leu Val Thr Leu Leu Lys Asp Glu Lys Val Tyr Glu
550                 555                 560                 565

acc cgc aaa ttc aat ctc gcg gaa ggc ctc gat ctt tcc cta aca ttc   1843
Thr Arg Lys Phe Asn Leu Ala Glu Gly Leu Asp Leu Ser Leu Thr Phe
                570                 575                 580

agc gga ggc gga cct gaa aat cga ttt agg tac ccc agc atc aat cag   1891
Ser Gly Gly Gly Pro Glu Asn Arg Phe Arg Tyr Pro Ser Ile Asn Gln
            585                 590                 595

gga caa act ggc tta aca aag act ttc gcc cgt ttt agt tcc aat tct   1939
Gly Gln Thr Gly Leu Thr Lys Thr Phe Ala Arg Phe Ser Ser Asn Ser
        600                 605                 610

gaa aag cac atc agg ttc cca gat gag atc atc ggg ctt gat gca ttc   1987
Glu Lys His Ile Arg Phe Pro Asp Glu Ile Ile Gly Leu Asp Ala Phe
    615                 620                 625

acc tct caa aaa gcg ttt aac atc gca agc ggt gat ttc cct gag gac   2035
Thr Ser Gln Lys Ala Phe Asn Ile Ala Ser Gly Asp Phe Pro Glu Asp
630                 635                 640                 645

tac aac ctc gac gtt ttc atc acg cct ccg caa ctt cac tac caa gta   2083
```

```
Tyr Asn Leu Asp Val Phe Ile Thr Pro Pro Gln Leu His Tyr Gln Val
                650                 655                 660

cct gtc aca cac agc caa aca aag tgg gaa agc aca aag acg aca cta   2131
Pro Val Thr His Ser Gln Thr Lys Trp Glu Ser Thr Lys Thr Thr Leu
            665                 670                 675

gat ttc aat gac ttt gcc gat gga aac ctc cag atc aga ttc cct aat   2179
Asp Phe Asn Asp Phe Ala Asp Gly Asn Leu Gln Ile Arg Phe Pro Asn
        680                 685                 690

gaa gtc tat gat cca aac ttg aaa atc att aaa atg gtg gca tac aag   2227
Glu Val Tyr Asp Pro Asn Leu Lys Ile Ile Lys Met Val Ala Tyr Lys
    695                 700                 705

aaa cct gag tcc agt gag cct aaa tac tta agc aaa att ggt tca agc   2275
Lys Pro Glu Ser Ser Glu Pro Lys Tyr Leu Ser Lys Ile Gly Ser Ser
710                 715                 720                 725

aaa gtg tgg tct atc cct atg gat cgc atc aag gaa ctc atg gat gat   2323
Lys Val Trp Ser Ile Pro Met Asp Arg Ile Lys Glu Leu Met Asp Asp
                730                 735                 740

gat gcc caa ttc ctt ttg atc gcg gag tgg ttc gct gaa agt aaa gac   2371
Asp Ala Gln Phe Leu Leu Ile Ala Glu Trp Phe Ala Glu Ser Lys Asp
            745                 750                 755

cag cac cga gag aag atc att agc gaa gct aag cga act gga aaa atc   2419
Gln His Arg Glu Lys Ile Ile Ser Glu Ala Lys Arg Thr Gly Lys Ile
        760                 765                 770

tcc aat gca gcg ctt aag agt gct cgt cct caa cct caa gca agt tcc   2467
Ser Asn Ala Ala Leu Lys Ser Ala Arg Pro Gln Pro Gln Ala Ser Ser
    775                 780                 785

cac att gca aca att gag aaa aag ccc cta cta gct gcg gct gaa att   2515
His Ile Ala Thr Ile Glu Lys Lys Pro Leu Leu Ala Ala Ala Glu Ile
790                 795                 800                 805

aag ctt tct acc gtg gag ttg gaa ctt ggt cgg cac act tct aag aga   2563
Lys Leu Ser Thr Val Glu Leu Glu Leu Gly Arg His Thr Ser Lys Arg
                810                 815                 820

ctg gaa ggc tgg gca tgg tct gcg ctc aac ccg ctt gat cca cca atc   2611
Leu Glu Gly Trp Ala Trp Ser Ala Leu Asn Pro Leu Asp Pro Pro Ile
            825                 830                 835

aaa gtc gat ttc caa gga acc tca ggc tca ctt cca gac acc cac ttc   2659
Lys Val Asp Phe Gln Gly Thr Ser Gly Ser Leu Pro Asp Thr His Phe
        840                 845                 850

gtc gtt ggc cct tta atc gtg gaa gtg aga gaa aaa gag ttt ctc tcc   2707
Val Val Gly Pro Leu Ile Val Glu Val Arg Glu Lys Glu Phe Leu Ser
    855                 860                 865

caa tgg cag cca aaa gtt ccc tca gtt aaa gcc gtg gtt gca aat gat   2755
Gln Trp Gln Pro Lys Val Pro Ser Val Lys Ala Val Val Ala Asn Asp
870                 875                 880                 885

ccc tca ttt gaa ttg gac cct caa ttt gat cct ttc ctc aca cac cga   2803
Pro Ser Phe Glu Leu Asp Pro Gln Phe Asp Pro Phe Leu Thr His Arg
```

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                890                 895                 900

tgg atg ttc gct cca cga agt ggg aag gtc tta ctc cca caa gaa atc   2851
Trp Met Phe Ala Pro Arg Ser Gly Lys Val Leu Leu Pro Gln Glu Ile
            905                 910                 915

cgc aca gtg tgg gac gcc cga ttc aat atg cgc cat gtc tta gcg cag   2899
Arg Thr Val Trp Asp Ala Arg Phe Asn Met Arg His Val Leu Ala Gln
        920                 925                 930

cgt gaa aac ctt cat gtg aaa tcg att caa gat ttt gac gat gcc acc   2947
Arg Glu Asn Leu His Val Lys Ser Ile Gln Asp Phe Asp Asp Ala Thr
    935                 940                 945

agt acc tat ctc acc agt gat cct cgg gtg gca tta gat gaa ttg gat   2995
Ser Thr Tyr Leu Thr Ser Asp Pro Arg Val Ala Leu Asp Glu Leu Asp
950                 955                 960                 965

aag agc tca att ccg tct aat tcc cac ttt gaa tca ttc atc cga tcc   3043
Lys Ser Ser Ile Pro Ser Asn Ser His Phe Glu Ser Phe Ile Arg Ser
                970                 975                 980

gga tta gct gag ctt tct ttc gaa gtt gac gac aca gcc gga gat atc   3091
Gly Leu Ala Glu Leu Ser Phe Glu Val Asp Asp Thr Ala Gly Asp Ile
            985                 990                 995

cat cgc gtt ccc tgg atc ggc ctg atc cag gaa atg aac gac ctc aga   3139
His Arg Val Pro Trp Ile Gly Leu Ile Gln Glu Met Asn Asp Leu Arg
        1000                1005                1010

att ctg cag ata caa ggc tat gaa aca gaa gaa cga gcc atc gaa cgc   3187
Ile Leu Gln Ile Gln Gly Tyr Glu Thr Glu Glu Arg Ala Ile Glu Arg
    1015                1020                1025

cga aat tcg cag agc tac atc cgt gag ata gga ggc agt gaa ttg tgg   3235
Arg Asn Ser Gln Ser Tyr Ile Arg Glu Ile Gly Gly Ser Glu Leu Trp
1030                1035                1040                1045

aat atc cta aaa gga aat tca gag gga ttg tct ctt gct caa aaa tgc   3283
Asn Ile Leu Lys Gly Asn Ser Glu Gly Leu Ser Leu Ala Gln Lys Cys
                1050                1055                1060

gca cca caa gcc act gag att aat gtg att cgt aat tca ggc ttg gaa   3331
Ala Pro Gln Ala Thr Glu Ile Asn Val Ile Arg Asn Ser Gly Leu Glu
            1065                1070                1075

gct atg cgc aat ggg ctg ggc gcc gat cag ttc agc gcc gag ttt att   3379
Ala Met Arg Asn Gly Leu Gly Ala Asp Gln Phe Ser Ala Glu Phe Ile
        1080                1085                1090

tca gca gac tca cgc cta cga gct cag ctt gaa tgg ttg gaa aac cgc   3427
Ser Ala Asp Ser Arg Leu Arg Ala Gln Leu Glu Trp Leu Glu Asn Arg
    1095                1100                1105

cga gag ctc aat gat ctc ggc cag ctc cca acg ctc ttc gat ttc gcc   3475
Arg Glu Leu Asn Asp Leu Gly Gln Leu Pro Thr Leu Phe Asp Phe Ala
1110                1115                1120                1125

gag aaa tac gag tac ctc atc gat cac tta ggt gat gat cgc atc aag   3523
Glu Lys Tyr Glu Tyr Leu Ile Asp His Leu Gly Asp Asp Arg Ile Lys
                1130                1135                1140
```

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gtc act gca cgt gag ctg tct act ctt gcg tcg gaa cac cgt cgc ggc   3571
Val Thr Ala Arg Glu Leu Ser Thr Leu Ala Ser Glu His Arg Arg Gly
            1145                1150                1155

aac gct gaa aac tgg ctt tat gca cca tat gtg tca ttc att tac agc   3619
Asn Ala Glu Asn Trp Leu Tyr Ala Pro Tyr Val Ser Phe Ile Tyr Ser
        1160                1165                1170

ttg ctt aac cga atg atc gct cat gaa gta ata cgt ccg atc gct cag   3667
Leu Leu Asn Arg Met Ile Ala His Glu Val Ile Arg Pro Ile Ala Gln
    1175                1180                1185

atc aat tac tca cgg cac gat tgg gca aac gct gct cgg ctg att cct   3715
Ile Asn Tyr Ser Arg His Asp Trp Ala Asn Ala Ala Arg Leu Ile Pro
1190                1195                1200                1205

cgt ctc aca gga ttt gac ctg gtg agt gcc gaa gcg aaa gtg ctc agc   3763
Arg Leu Thr Gly Phe Asp Leu Val Ser Ala Glu Ala Lys Val Leu Ser
                1210                1215                1220

gca ata aac aac aac aat ata atc cca act gca att taaggatcac        3809
Ala Ile Asn Asn Asn Asn Ile Ile Pro Thr Ala Ile
            1225                1230

tatgtccaac gca                                                   3822


<210> 2698
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<213> Corynebacterium glutamicum

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Val Thr Ile Ser Arg Arg Leu Lys Gln Glu Arg Ser Phe Ala Asp Asp
  1               5                  10                  15

Leu Gln Asp Leu Lys Thr Leu Asn Asp Gln Leu Arg Phe Thr Asn Ala
             20                  25                  30

Lys Leu Gln Ala Arg Ile Ser Gly Ile Gly Asn Asp Gly Lys Lys Ile
         35                  40                  45

Thr Arg Pro Thr Pro Leu Leu Ala Leu Asp Phe Gln Leu Thr Val Glu
     50                  55                  60

Glu Tyr Glu Thr Ile Ile Ala Ile Leu Val Glu Ala Val Gly Gly Asn
 65                  70                  75                  80

Gln Ser Lys Pro Ala Ile Leu Lys Asp Leu Phe Ile Glu Tyr Pro Leu
                 85                  90                  95

Val Phe Leu Ala Ala Leu Ser Gly Thr Ala Met Leu Asp Ala Gln Glu
            100                 105                 110

Gly Phe Trp Pro Ala Phe Trp Lys Arg Thr Gln Val Ser Val Pro Glu
        115                 120                 125

His Val Tyr Asp Ala Ile Arg Lys Glu Leu Val Asn Ser Ile Arg Lys
    130                 135                 140
```

```
Asn Gly Leu Glu Thr Phe Ser Leu Ala Asp Leu Asn Arg Arg Glu Tyr
145                 150                 155                 160

Val Gly Leu Ile Gln Leu His Ser Gly Leu Ser Ala Lys Asp Met Leu
                165                 170                 175

Ala Leu Val Lys Phe Ile Asp His Thr Arg Ala Glu Asn Gln Gly Trp
            180                 185                 190

Asp Ser Gly Glu Asp Phe Ala Ser Tyr Ala Lys Ser Val Phe Ser Ser
        195                 200                 205

Gly Asp Asn Leu Leu Thr Thr Glu Ser Leu Lys Gln Leu Val Thr His
    210                 215                 220

Ile Pro Ala Arg Ser Val Asp Phe Ile Ala Arg Val Tyr Glu Leu Thr
225                 230                 235                 240

Asn Trp Tyr Arg Asp Leu Lys Asp Leu Asn Glu Val Glu Ala Phe Val
                245                 250                 255

Gly Thr His Gly Leu Pro Glu Leu Ser Phe Lys Phe Leu Leu Glu Cys
            260                 265                 270

Leu Ser Gly Glu Ala Glu Gln Ile Ala Glu Lys Thr Lys Ala Ala Pro
        275                 280                 285

Ala Ser Leu Glu Asn Leu Glu Pro Pro His Leu Tyr Leu Asp Pro Gln
    290                 295                 300

Ser Phe Glu Leu Ser Leu Val Phe Pro Ala Ile Ser Lys Thr Ala Ala
305                 310                 315                 320

Leu Gln Ile Pro Ala Pro Glu Trp Thr Val Ile Tyr Asp Gly Asn Ser
                325                 330                 335

Ile Lys Val Arg Pro Glu Gln Asp Trp Ser Tyr Gly Gly Phe Ala Glu
            340                 345                 350

Tyr Arg Leu Pro Leu Asp Lys Pro Leu Ser Ser Leu Arg Val Ile Thr
        355                 360                 365

Pro Thr Glu Lys Ser Leu Ile Leu Ile Glu Gly Phe Gly His Lys Asn
    370                 375                 380

Pro Ile Met Phe Phe Lys Asn Asn Gly Gln Pro Tyr Ala Asn Gln Glu
385                 390                 395                 400

Met Leu Ser Gly Asn Ala Val Thr Ala Ile Val Pro Ala Ala Ala Ile
                405                 410                 415

Ile Arg Ala Arg Met Arg Ala Ser Lys Thr Phe Asn Tyr Gln Asp Leu
            420                 425                 430

Gly Pro Leu Ser Gly Trp Asn Lys Trp Val Ile Arg Ser Ile Pro Leu
        435                 440                 445

Lys Arg Ala Glu Ser Ile Thr Val Ser His Gly Gly Phe Arg Lys Glu
    450                 455                 460

Leu Pro Val Arg Arg Lys Val Asp Val Gln Trp Ile Thr Glu Asp Leu
```

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465                 470                 475                 480

Thr Ile Glu Asn Leu Gln Gly Leu Asp His Glu Pro Val Phe His Thr
                485                 490                 495

Ser Pro Arg Ile Glu Phe Pro Thr Ser Gly Ser Asn Trp Val Ile Gln
            500                 505                 510

Tyr Ser Gln Ile Leu Pro Asp Gly Ser Leu Ile Glu Met Glu Asp Tyr
        515                 520                 525

Pro Val Glu Pro Glu Asn Phe Gly Tyr Glu Leu Asp Leu Phe Glu Glu
    530                 535                 540

Ser Asp Asp Pro Trp Val Gly Gln Phe Leu Val Thr Leu Leu Lys Asp
545                 550                 555                 560

Glu Lys Val Tyr Glu Thr Arg Lys Phe Asn Leu Ala Glu Gly Leu Asp
                565                 570                 575

Leu Ser Leu Thr Phe Ser Gly Gly Gly Pro Glu Asn Arg Phe Arg Tyr
            580                 585                 590

Pro Ser Ile Asn Gln Gly Gln Thr Gly Leu Thr Lys Thr Phe Ala Arg
        595                 600                 605

Phe Ser Ser Asn Ser Glu Lys His Ile Arg Phe Pro Asp Glu Ile Ile
    610                 615                 620

Gly Leu Asp Ala Phe Thr Ser Gln Lys Ala Phe Asn Ile Ala Ser Gly
625                 630                 635                 640

Asp Phe Pro Glu Asp Tyr Asn Leu Asp Val Phe Ile Thr Pro Pro Gln
                645                 650                 655

Leu His Tyr Gln Val Pro Val Thr His Ser Gln Thr Lys Trp Glu Ser
            660                 665                 670

Thr Lys Thr Thr Leu Asp Phe Asn Asp Phe Ala Asp Gly Asn Leu Gln
        675                 680                 685

Ile Arg Phe Pro Asn Glu Val Tyr Asp Pro Asn Leu Lys Ile Ile Lys
    690                 695                 700

Met Val Ala Tyr Lys Lys Pro Glu Ser Ser Glu Pro Lys Tyr Leu Ser
705                 710                 715                 720

Lys Ile Gly Ser Ser Lys Val Trp Ser Ile Pro Met Asp Arg Ile Lys
                725                 730                 735

Glu Leu Met Asp Asp Asp Ala Gln Phe Leu Leu Ile Ala Glu Trp Phe
            740                 745                 750

Ala Glu Ser Lys Asp Gln His Arg Glu Lys Ile Ile Ser Glu Ala Lys
        755                 760                 765

Arg Thr Gly Lys Ile Ser Asn Ala Ala Leu Lys Ser Ala Arg Pro Gln
    770                 775                 780

Pro Gln Ala Ser Ser His Ile Ala Thr Ile Glu Lys Lys Pro Leu Leu
785                 790                 795                 800
```

```
Ala Ala Ala Glu Ile Lys Leu Ser Thr Val Glu Leu Glu Leu Gly Arg
                805                 810                 815

His Thr Ser Lys Arg Leu Glu Gly Trp Ala Trp Ser Ala Leu Asn Pro
            820                 825                 830

Leu Asp Pro Pro Ile Lys Val Asp Phe Gln Gly Thr Ser Gly Ser Leu
        835                 840                 845

Pro Asp Thr His Phe Val Val Gly Pro Leu Ile Val Glu Val Arg Glu
    850                 855                 860

Lys Glu Phe Leu Ser Gln Trp Gln Pro Lys Val Pro Ser Val Lys Ala
865                 870                 875                 880

Val Val Ala Asn Asp Pro Ser Phe Glu Leu Asp Pro Gln Phe Asp Pro
                885                 890                 895

Phe Leu Thr His Arg Trp Met Phe Ala Pro Arg Ser Gly Lys Val Leu
            900                 905                 910

Leu Pro Gln Glu Ile Arg Thr Val Trp Asp Ala Arg Phe Asn Met Arg
        915                 920                 925

His Val Leu Ala Gln Arg Glu Asn Leu His Val Lys Ser Ile Gln Asp
    930                 935                 940

Phe Asp Asp Ala Thr Ser Thr Tyr Leu Thr Ser Asp Pro Arg Val Ala
945                 950                 955                 960

Leu Asp Glu Leu Asp Lys Ser Ser Ile Pro Ser Asn Ser His Phe Glu
                965                 970                 975

Ser Phe Ile Arg Ser Gly Leu Ala Glu Leu Ser Phe Glu Val Asp Asp
            980                 985                 990

Thr Ala Gly Asp Ile His Arg Val Pro Trp Ile Gly Leu Ile Gln Glu
        995                1000                1005

Met Asn Asp Leu Arg Ile Leu Gln Ile Gln Gly Tyr Glu Thr Glu Glu
    1010                1015                1020

Arg Ala Ile Glu Arg Arg Asn Ser Gln Ser Tyr Ile Arg Glu Ile Gly
1025                1030                1035                1040

Gly Ser Glu Leu Trp Asn Ile Leu Lys Gly Asn Ser Glu Gly Leu Ser
                1045                1050                1055

Leu Ala Gln Lys Cys Ala Pro Gln Ala Thr Glu Ile Asn Val Ile Arg
            1060                1065                1070

Asn Ser Gly Leu Glu Ala Met Arg Asn Gly Leu Gly Ala Asp Gln Phe
        1075                1080                1085

Ser Ala Glu Phe Ile Ser Ala Asp Ser Arg Leu Arg Ala Gln Leu Glu
    1090                1095                1100

Trp Leu Glu Asn Arg Arg Glu Leu Asn Asp Leu Gly Gln Leu Pro Thr
1105                1110                1115                1120
```

```
Leu Phe Asp Phe Ala Glu Lys Tyr Glu Tyr Leu Ile Asp His Leu Gly
                1125                1130                1135

Asp Asp Arg Ile Lys Val Thr Ala Arg Glu Leu Ser Thr Leu Ala Ser
            1140                1145                1150

Glu His Arg Arg Gly Asn Ala Glu Asn Trp Leu Tyr Ala Pro Tyr Val
        1155                1160                1165

Ser Phe Ile Tyr Ser Leu Leu Asn Arg Met Ile Ala His Glu Val Ile
    1170                1175                1180

Arg Pro Ile Ala Gln Ile Asn Tyr Ser Arg His Asp Trp Ala Asn Ala
1185                1190                1195                1200

Ala Arg Leu Ile Pro Arg Leu Thr Gly Phe Asp Leu Val Ser Ala Glu
                1205                1210                1215

Ala Lys Val Leu Ser Ala Ile Asn Asn Asn Asn Ile Ile Pro Thr Ala
            1220                1225                1230

Ile
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20220228 US 63154744 20210301

<210> 2699
<211> 744
<212> DNA
<213> Corynebacterium glutamicum

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<221> CDS
<222> (101)..(721)
<223> RXA02374

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attggatagc ccaccgtacg cctatctaca ctgaattacc atg agc tat gac ttt 115
                                          Met Ser Tyr Asp Phe
                                            1   5

gtc ctc ttt gaa acc gat ggc gac cca ggt agc gcc cgt att tcc aaa 163
Val Leu Phe Glu Thr Asp Gly Asp Pro Gly Ser Ala Arg Ile Ser Lys
                10   15   20

acc cca ctg acc gaa cgc atc gat ttc gcc acg cca tct aca acc cct 211
Thr Pro Leu Thr Glu Arg Ile Asp Phe Ala Thr Pro Ser Thr Thr Pro
            25   30   35

gtg ttg gaa tct ctt tcg gca ggg ctt gcc gaa acg gtg cca gac acc 259
Val Leu Glu Ser Leu Ser Ala Gly Leu Ala Glu Thr Val Pro Asp Thr
        40   45   50

gtc aag ctt gaa gaa gac gcc atc cac tta tcc ggt gat cgt tgc ctt 307
Val Lys Leu Glu Glu Asp Ala Ile His Leu Ser Gly Asp Arg Cys Leu
    55   60   65

tac gtt gtg acc aac tac aac tcc gcc gaa gaa gca gcc gaa tgg ctc 355
Tyr Val Val Thr Asn Tyr Asn Ser Ala Glu Glu Ala Ala Glu Trp Leu
70   75   80   85
```
```

```
acc gcc atc gct ttc gat tac gga ctg ggc ctt gcc gac atg aac gcg   403
Thr Ala Ile Ala Phe Asp Tyr Gly Leu Gly Leu Ala Asp Met Asn Ala
                 90                  95                 100

gac acc atc ctg ctt ttc ggc gat gaa gat tcc gac gct gtc gtc caa   451
Asp Thr Ile Leu Leu Phe Gly Asp Glu Asp Ser Asp Ala Val Val Gln
            105                 110                 115

atc gat gac tgg ttc tcc ccc gct ttc tct gcg tac ggc ctt ccc cac   499
Ile Asp Asp Trp Phe Ser Pro Ala Phe Ser Ala Tyr Gly Leu Pro His
        120                 125                 130

ctc ctg gtg gaa gtc atg cgc ctg aag gat tcc aaa acc cct tat ctt   547
Leu Leu Val Glu Val Met Arg Leu Lys Asp Ser Lys Thr Pro Tyr Leu
    135                 140                 145

cga gtc aca ctt gct gca gat gac tcg aaa ttt atc caa acc ctt tac   595
Arg Val Thr Leu Ala Ala Asp Asp Ser Lys Phe Ile Gln Thr Leu Tyr
150                 155                 160                 165

gaa acc gac aac aaa caa tgg ttg gtg gaa acc tct tcc tcc aca ggc   643
Glu Thr Asp Asn Lys Gln Trp Leu Val Glu Thr Ser Ser Ser Thr Gly
                170                 175                 180

acg gac gaa acc cac gtg aag acc att aat gat gtg ctg gaa cgc atc   691
Thr Asp Glu Thr His Val Lys Thr Ile Asn Asp Val Leu Glu Arg Ile
            185                 190                 195

gag aca tgg ttc aac cag gag act gct gtc taaacctttt gtcgtgttct     741
Glu Thr Trp Phe Asn Gln Glu Thr Ala Val
        200                 205

ggg                                                               744


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<213> Corynebacterium glutamicum

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Met Ser Tyr Asp Phe Val Leu Phe Glu Thr Asp Gly Asp Pro Gly Ser
  1               5                  10                  15

Ala Arg Ile Ser Lys Thr Pro Leu Thr Glu Arg Ile Asp Phe Ala Thr
             20                  25                  30

Pro Ser Thr Thr Pro Val Leu Glu Ser Leu Ser Ala Gly Leu Ala Glu
         35                  40                  45

Thr Val Pro Asp Thr Val Lys Leu Glu Glu Asp Ala Ile His Leu Ser
     50                  55                  60

Gly Asp Arg Cys Leu Tyr Val Val Thr Asn Tyr Asn Ser Ala Glu Glu
 65                  70                  75                  80

Ala Ala Glu Trp Leu Thr Ala Ile Ala Phe Asp Tyr Gly Leu Gly Leu
                 85                  90                  95

Ala Asp Met Asn Ala Asp Thr Ile Leu Leu Phe Gly Asp Glu Asp Ser
```

```
            100                 105                 110

Asp Ala Val Val Gln Ile Asp Asp Trp Phe Ser Pro Ala Phe Ser Ala
        115                 120                 125

Tyr Gly Leu Pro His Leu Leu Val Glu Val Met Arg Leu Lys Asp Ser
    130                 135                 140

Lys Thr Pro Tyr Leu Arg Val Thr Leu Ala Ala Asp Asp Ser Lys Phe
145                 150                 155                 160

Ile Gln Thr Leu Tyr Glu Thr Asp Asn Lys Gln Trp Leu Val Glu Thr
                165                 170                 175

Ser Ser Ser Thr Gly Thr Asp Glu Thr His Val Lys Thr Ile Asn Asp
            180                 185                 190

Val Leu Glu Arg Ile Glu Thr Trp Phe Asn Gln Glu Thr Ala Val
        195                 200                 205
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<222> (101)..(769)
<223> RXA02390

<400> 2701

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ggccgcgagg atctcgtagc tcgcttcgag tcataggccg gtg gag tgg acc gct   115
                                            Val Glu Trp Thr Ala
                                              1               5

ttt ggc acc ctg att ctg ctc aat ttg gtg ggc agt tta tcc ccg ggg   163
Phe Gly Thr Leu Ile Leu Leu Asn Leu Val Gly Ser Leu Ser Pro Gly
                10                  15                  20

cct gat acc ttt ttc ctc ctc cgc tta gcc acc cgc tcc aga gcg cac   211
Pro Asp Thr Phe Phe Leu Leu Arg Leu Ala Thr Arg Ser Arg Ala His
            25                  30                  35

gcg atc gct ggc gtc gcc ggc atc gtc acc gga ctc acg gtg tgg gtg   259
Ala Ile Ala Gly Val Ala Gly Ile Val Thr Gly Leu Thr Val Trp Val
        40                  45                  50

acg ctg acg gtc gtg gga gca gcg gcg ctg ctc acc act tat ccg tcg   307
Thr Leu Thr Val Val Gly Ala Ala Ala Leu Leu Thr Thr Tyr Pro Ser
    55                  60                  65

att ctc gga atc atc cag ctc gtc ggc ggc acg tac cta agc ttc att   355
Ile Leu Gly Ile Ile Gln Leu Val Gly Gly Thr Tyr Leu Ser Phe Ile
70                  75                  80                  85

ggg tac aag ttg ctg cgc tcg gcg tcg aga gag ctt atc gac gcc cgc   403
Gly Tyr Lys Leu Leu Arg Ser Ala Ser Arg Glu Leu Ile Asp Ala Arg
                90                  95                  100
```

```
cag ttc cgt ttc aac gcc gat gcc cga cct atc ccg gat gcg gta gaa   451
Gln Phe Arg Phe Asn Ala Asp Ala Arg Pro Ile Pro Asp Ala Val Glu
            105                 110                 115

gca ctg gga acc cgc act cag gta tat cga caa ggt ttg gcc acc aac   499
Ala Leu Gly Thr Arg Thr Gln Val Tyr Arg Gln Gly Leu Ala Thr Asn
        120                 125                 130

ctg tca aac cct aaa gtt gtc atg tac ttc gcg gca att ctg gct ccg   547
Leu Ser Asn Pro Lys Val Val Met Tyr Phe Ala Ala Ile Leu Ala Pro
    135                 140                 145

ttg atg cca gcg cac cca tca ccg gtg ctg gcg ttc tct atc atc gtg   595
Leu Met Pro Ala His Pro Ser Pro Val Leu Ala Phe Ser Ile Ile Val
150                 155                 160                 165

gcg att tta gtg cag acc ttt gtt acc ttc tct gct gtg tgc ctc att   643
Ala Ile Leu Val Gln Thr Phe Val Thr Phe Ser Ala Val Cys Leu Ile
                170                 175                 180

gtc tct acg gag cgt gtg cgc aaa gca atg ctg cgt gca ggt ccc tgg   691
Val Ser Thr Glu Arg Val Arg Lys Ala Met Leu Arg Ala Gly Pro Trp
            185                 190                 195

ttt gac ctg ctt gct ggc gtt gtc ttc ctc gtt gtg ggt gtg act ctg   739
Phe Asp Leu Leu Ala Gly Val Val Phe Leu Val Val Gly Val Thr Leu
        200                 205                 210

ctg tat gaa ggc ctg acc ggt tta ctc ggg taaaggcata aaaaatggct     789
Leu Tyr Glu Gly Leu Thr Gly Leu Leu Gly
    215                 220

tcc                                                               792


<210> 2702
<211> 223
<212> PRT
<213> Corynebacterium glutamicum

<400> 2702
Val Glu Trp Thr Ala Phe Gly Thr Leu Ile Leu Leu Asn Leu Val Gly
  1               5                  10                  15

Ser Leu Ser Pro Gly Pro Asp Thr Phe Phe Leu Leu Arg Leu Ala Thr
             20                  25                  30

Arg Ser Arg Ala His Ala Ile Ala Gly Val Ala Gly Ile Val Thr Gly
         35                  40                  45

Leu Thr Val Trp Val Thr Leu Thr Val Val Gly Ala Ala Ala Leu Leu
     50                  55                  60

Thr Thr Tyr Pro Ser Ile Leu Gly Ile Ile Gln Leu Val Gly Gly Thr
 65                  70                  75                  80

Tyr Leu Ser Phe Ile Gly Tyr Lys Leu Leu Arg Ser Ala Ser Arg Glu
                 85                  90                  95

Leu Ile Asp Ala Arg Gln Phe Arg Phe Asn Ala Asp Ala Arg Pro Ile
```

```
            100                 105                 110

Pro Asp Ala Val Glu Ala Leu Gly Thr Arg Thr Gln Val Tyr Arg Gln
        115                 120                 125

Gly Leu Ala Thr Asn Leu Ser Asn Pro Lys Val Val Met Tyr Phe Ala
    130                 135                 140

Ala Ile Leu Ala Pro Leu Met Pro Ala His Pro Ser Pro Val Leu Ala
145                 150                 155                 160

Phe Ser Ile Ile Val Ala Ile Leu Val Gln Thr Phe Val Thr Phe Ser
                165                 170                 175

Ala Val Cys Leu Ile Val Ser Thr Glu Arg Val Arg Lys Ala Met Leu
            180                 185                 190

Arg Ala Gly Pro Trp Phe Asp Leu Leu Ala Gly Val Val Phe Leu Val
        195                 200                 205

Val Gly Val Thr Leu Leu Tyr Glu Gly Leu Thr Gly Leu Leu Gly
    210                 215                 220
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Sequence Listing Free Text

<210> 2703
<211> 405
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(382)
<223> RXA02393

<400> 2703

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gccaccttca tttttcncan gccncngcaa atcagaacnc naccttctgg cactcccngc 60

tcaaatnngg gacgtccatg cngangtttt agacatcttc atg gcg gaa tct tta   115
                                            Met Ala Glu Ser Leu
                                              1               5

gtg att atc aac atc gac gag aaa agc gcc aag ctg ctt atc gac gcc   163
Val Ile Ile Asn Ile Asp Glu Lys Ser Ala Lys Leu Leu Ile Asp Ala
                 10                  15                  20

gcc cgc cac cac atc ccc acc cgc ttc acc ggg ccc aac gcc cgg ccg   211
Ala Arg His His Ile Pro Thr Arg Phe Thr Gly Pro Asn Ala Arg Pro
             25                  30                  35

ctc agc gtc atc ccc atc gag gat ccc cgc tca cgc ccg acg ctc cac   259
Leu Ser Val Ile Pro Ile Glu Asp Pro Arg Ser Arg Pro Thr Leu His
         40                  45                  50

cca gat cat ggt tgg atg atg ccg cta agc cca cca gtg gtg gat gaa   307
Pro Asp His Gly Trp Met Met Pro Leu Ser Pro Pro Val Val Asp Glu
     55                  60                  65

ctg ctt ggc ggt ggc ttg aaa att gga gaa aca gaa cta gaa agc acc   355
Leu Leu Gly Gly Gly Leu Lys Ile Gly Glu Thr Glu Leu Glu Ser Thr
 70                  75                  80                  85
```

```
aac att gcg ttc att gtt gat gct tcc taaaaatcct gtgccgtgag          402
Asn Ile Ala Phe Ile Val Asp Ala Ser
                 90

gtt                                                                405


<210> 2704
<211> 94
<212> PRT
<213> Corynebacterium glutamicum

<400> 2704
Met Ala Glu Ser Leu Val Ile Ile Asn Ile Asp Glu Lys Ser Ala Lys
  1               5                  10                  15

Leu Leu Ile Asp Ala Ala Arg His His Ile Pro Thr Arg Phe Thr Gly
             20                  25                  30

Pro Asn Ala Arg Pro Leu Ser Val Ile Pro Ile Glu Asp Pro Arg Ser
         35                  40                  45

Arg Pro Thr Leu His Pro Asp His Gly Trp Met Met Pro Leu Ser Pro
     50                  55                  60

Pro Val Val Asp Glu Leu Leu Gly Gly Gly Leu Lys Ile Gly Glu Thr
 65                  70                  75                  80

Glu Leu Glu Ser Thr Asn Ile Ala Phe Ile Val Asp Ala Ser
                 85                  90


<210> 2705
<211> 755
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(732)
<223> RXA02395

<400> 2705
ctc atc acc atg gct atc ccc tcc ttc att ttg atc ctg gcg ttc acc   48
Leu Ile Thr Met Ala Ile Pro Ser Phe Ile Leu Ile Leu Ala Phe Thr
  1               5                  10                  15

att ttc ggt gga act gcc atc acg atg aac cgc gag aac gta gat ggt   96
Ile Phe Gly Gly Thr Ala Ile Thr Met Asn Arg Glu Asn Val Asp Gly
             20                  25                  30

ttt gac ggc agt tca tcc aag gaa cag gtg ctg ttt gat atg ttc agc   144
Phe Asp Gly Ser Ser Ser Lys Glu Gln Val Leu Phe Asp Met Phe Ser
         35                  40                  45

aac ctt ccg ctg tac tcg atc aca ccg ttc att ttg atc ttt gtg ctg   192
Asn Leu Pro Leu Tyr Ser Ile Thr Pro Phe Ile Leu Ile Phe Val Leu
     50                  55                  60

gca gta ttc ttt gtt acc tct gcc gat tcc gcc tcc gtg gtg atg gga   240
Ala Val Phe Phe Val Thr Ser Ala Asp Ser Ala Ser Val Val Met Gly
```

```
 65                  70                  75                  80

acg atg agc tcc caa ggt aac cct gca cca aac aaa tta atc gtg gtg   288
Thr Met Ser Ser Gln Gly Asn Pro Ala Pro Asn Lys Leu Ile Val Val
                 85                  90                  95

ttc tgg gga ctg tgc atg atg ggc atc gcg gtg gtc atg ctg ctt act   336
Phe Trp Gly Leu Cys Met Met Gly Ile Ala Val Val Met Leu Leu Thr
            100                 105                 110

ggt ggc gaa tcc gcg ctg act ggt ctg cag aac ctc acc att ttg atc   384
Gly Gly Glu Ser Ala Leu Thr Gly Leu Gln Asn Leu Thr Ile Leu Ile
        115                 120                 125

gcc att ccg ttt gcg ctg gtg ttg atc gtg atg gct att gcc ttt att   432
Ala Ile Pro Phe Ala Leu Val Leu Ile Val Met Ala Ile Ala Phe Ile
    130                 135                 140

aag gac tta tcc aca gac cca gcc gct att cga caa cgc tat gca aag   480
Lys Asp Leu Ser Thr Asp Pro Ala Ala Ile Arg Gln Arg Tyr Ala Lys
145                 150                 155                 160

gca gcc atc tct aac gcg gtg gtt cgt ggc ttg gaa gaa cac ggc gac   528
Ala Ala Ile Ser Asn Ala Val Val Arg Gly Leu Glu Glu His Gly Asp
                165                 170                 175

gac ttc gag ctc tcc atc gaa cct gca gag gaa ggt cgt gga gcg ggt   576
Asp Phe Glu Leu Ser Ile Glu Pro Ala Glu Glu Gly Arg Gly Ala Gly
            180                 185                 190

gct acc ttc gat tcc acc gct gat cac atc acc gac tgg tat cag cgc   624
Ala Thr Phe Asp Ser Thr Ala Asp His Ile Thr Asp Trp Tyr Gln Arg
        195                 200                 205

acc gac gaa gaa ggc aat gat gtt gat tat gac ttc acc acc ggc aaa   672
Thr Asp Glu Glu Gly Asn Asp Val Asp Tyr Asp Phe Thr Thr Gly Lys
    210                 215                 220

tgg gcc gat ggt tgg aca ccg gaa tcg acc gaa gaa ggc gaa gtg gac   720
Trp Ala Asp Gly Trp Thr Pro Glu Ser Thr Glu Glu Gly Glu Val Asp
225                 230                 235                 240

gcg aaa aag gat taaaaaataa cgactggctg gga                        755
Ala Lys Lys Asp
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<210> 2706
<211> 244
<212> PRT
<213> Corynebacterium glutamicum

<400> 2706

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Leu Ile Thr Met Ala Ile Pro Ser Phe Ile Leu Ile Leu Ala Phe Thr
  1               5                  10                  15

Ile Phe Gly Gly Thr Ala Ile Thr Met Asn Arg Glu Asn Val Asp Gly
             20                  25                  30

Phe Asp Gly Ser Ser Ser Lys Glu Gln Val Leu Phe Asp Met Phe Ser
         35                  40                  45
```

```
Asn Leu Pro Leu Tyr Ser Ile Thr Pro Phe Ile Leu Ile Phe Val Leu
     50                  55                  60

Ala Val Phe Phe Val Thr Ser Ala Asp Ser Ala Ser Val Val Met Gly
 65                  70                  75                  80

Thr Met Ser Ser Gln Gly Asn Pro Ala Pro Asn Lys Leu Ile Val Val
                 85                  90                  95

Phe Trp Gly Leu Cys Met Met Gly Ile Ala Val Val Met Leu Leu Thr
            100                 105                 110

Gly Gly Glu Ser Ala Leu Thr Gly Leu Gln Asn Leu Thr Ile Leu Ile
        115                 120                 125

Ala Ile Pro Phe Ala Leu Val Leu Ile Val Met Ala Ile Ala Phe Ile
    130                 135                 140

Lys Asp Leu Ser Thr Asp Pro Ala Ala Ile Arg Gln Arg Tyr Ala Lys
145                 150                 155                 160

Ala Ala Ile Ser Asn Ala Val Val Arg Gly Leu Glu Glu His Gly Asp
                165                 170                 175

Asp Phe Glu Leu Ser Ile Glu Pro Ala Glu Glu Gly Arg Gly Ala Gly
            180                 185                 190

Ala Thr Phe Asp Ser Thr Ala Asp His Ile Thr Asp Trp Tyr Gln Arg
        195                 200                 205

Thr Asp Glu Glu Gly Asn Asp Val Asp Tyr Asp Phe Thr Thr Gly Lys
    210                 215                 220

Trp Ala Asp Gly Trp Thr Pro Glu Ser Thr Glu Glu Gly Glu Val Asp
225                 230                 235                 240

Ala Lys Lys Asp
```

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<210> 2707
<211> 402
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(379)
<223> RXA02396

<400> 2707
gagtgcttgt aggttgatag aaagtaaact aaagtaaaca tcaggttaac agccgggggt 60

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tcaagtatta actccctcgg aaacagaaag gaacacgaca atg gct acc aca gct   115
                                              Met Ala Thr Thr Ala
                                                1               5

tcc aag atc tcc acg atc cgt cca gca cag caa gat gct ctt tgg agc   163
Ser Lys Ile Ser Thr Ile Arg Pro Ala Gln Gln Asp Ala Leu Trp Ser
                10                  15                  20
```

```
gta cgt gag gat ctt cac gct cgc ttc gat ggc ctg gtc gat cct gtc   211
Val Arg Glu Asp Leu His Ala Arg Phe Asp Gly Leu Val Asp Pro Val
             25                  30                  35

cag gta gac gca att ttg gac cat gtc gca tct aac cgc gaa gcc aag   259
Gln Val Asp Ala Ile Leu Asp His Val Ala Ser Asn Arg Glu Ala Lys
         40                  45                  50

atc acc gtc ttc agc aag att ttc atc gct cgc gag gca acc gct gca   307
Ile Thr Val Phe Ser Lys Ile Phe Ile Ala Arg Glu Ala Thr Ala Ala
     55                  60                  65

ctt cag cag att gct ggc aac gtt aac gca gac ctg ctt gac ttc att   355
Leu Gln Gln Ile Ala Gly Asn Val Asn Ala Asp Leu Leu Asp Phe Ile
 70                  75                  80                  85

gcc ctc aac cgt ggc atg gca gca taagttttag ctgcccataa att         402
Ala Leu Asn Arg Gly Met Ala Ala
                 90
```

Sequence Listing

<210> 2708
<211> 93
<212> PRT
<213> Corynebacterium glutamicum

<400> 2708

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Met Ala Thr Thr Ala Ser Lys Ile Ser Thr Ile Arg Pro Ala Gln Gln
  1               5                  10                  15

Asp Ala Leu Trp Ser Val Arg Glu Asp Leu His Ala Arg Phe Asp Gly
             20                  25                  30

Leu Val Asp Pro Val Gln Val Asp Ala Ile Leu Asp His Val Ala Ser
         35                  40                  45

Asn Arg Glu Ala Lys Ile Thr Val Phe Ser Lys Ile Phe Ile Ala Arg
     50                  55                  60

Glu Ala Thr Ala Ala Leu Gln Gln Ile Ala Gly Asn Val Asn Ala Asp
 65                  70                  75                  80

Leu Leu Asp Phe Ile Ala Leu Asn Arg Gly Met Ala Ala
                 85                  90
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<210> 2709
<211> 888
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(865)
<223> RXA02403

<400> 2709

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gcacagaatt aaatcgctgg tgtgcgaact ttcatacctt aacgcagtag tgatgcttaa 60

ggcacaacgt gggggcaatt ccggcctata ctttggaagt atg act act ttt att   115
```

```
                                                    Met Thr Thr Phe Ile
                                                      1               5

acc tcc ggt ggc ttg gaa atc tcc ccc gct ggc gct cat att gtt cac   163
Thr Ser Gly Gly Leu Glu Ile Ser Pro Ala Gly Ala His Ile Val His
                 10                  15                  20

gcc gaa tca cct gaa ggt gag ctg ttg ttt gtt agc tcc gct tcc caa   211
Ala Glu Ser Pro Glu Gly Glu Leu Leu Phe Val Ser Ser Ala Ser Gln
             25                  30                  35

tat ggg gag gga aat gca att agg ggt ggt gtg ccc atc att gct cca   259
Tyr Gly Glu Gly Asn Ala Ile Arg Gly Gly Val Pro Ile Ile Ala Pro
         40                  45                  50

tgg ttt ggt gga ctg ctt ggt ttg gac cct gca cat ggt tgg gcg aag   307
Trp Phe Gly Gly Leu Leu Gly Leu Asp Pro Ala His Gly Trp Ala Lys
     55                  60                  65

cgt tcc gcg tgg gac gtg act gaa cat gac ggc caa att cac gct gaa   355
Arg Ser Ala Trp Asp Val Thr Glu His Asp Gly Gln Ile His Ala Glu
 70                  75                  80                  85

tat ggc cgc gat ggt tta ctg ctg gat att cgt gcg aac agc act aag   403
Tyr Gly Arg Asp Gly Leu Leu Leu Asp Ile Arg Ala Asn Ser Thr Lys
                 90                  95                 100

aat ggt ttt gag atc acc ctg cgc gct tac aac gac acc gat gag gca   451
Asn Gly Phe Glu Ile Thr Leu Arg Ala Tyr Asn Asp Thr Asp Glu Ala
             105                 110                 115

cgc act gtg cag ttg gcc ttc cac cct tat ttc aag gtg gat gat gta   499
Arg Thr Val Gln Leu Ala Phe His Pro Tyr Phe Lys Val Asp Asp Val
         120                 125                 130

gaa aag atc gag gtc cgt ggc ctt gat ggg gtg gac att ctc aat cgc   547
Glu Lys Ile Glu Val Arg Gly Leu Asp Gly Val Asp Ile Leu Asn Arg
     135                 140                 145

ctg aac aat gag gtg gag acc caa gat ggt ccc gtt act ttt gat ggc   595
Leu Asn Asn Glu Val Glu Thr Gln Asp Gly Pro Val Thr Phe Asp Gly
150                 155                 160                 165

gag ttc gat cgc att gcg cta ggg act ccg gtt gtg agg att ttt gat   643
Glu Phe Asp Arg Ile Ala Leu Gly Thr Pro Val Val Arg Ile Phe Asp
                 170                 175                 180

acc gat cgc atc atc acc att gag ggc gat ggt cat gat tcc act gtg   691
Thr Asp Arg Ile Ile Thr Ile Glu Gly Asp Gly His Asp Ser Thr Val
             185                 190                 195

gtg tgg aat cca ggc gaa agt cgc gcc tcc acc gtg gcc gat att ggc   739
Val Trp Asn Pro Gly Glu Ser Arg Ala Ser Thr Val Ala Asp Ile Gly
         200                 205                 210

gaa ggt gaa tgg cgc gac ttt gtg tgt gtt gaa ccg gcg ctt ttg ggt   787
Glu Gly Glu Trp Arg Asp Phe Val Cys Val Glu Pro Ala Leu Leu Gly
     215                 220                 225

gct gac caa aaa gga gtg agg gtg gct ccg ggg cag tca gtc acc gtt   835
Ala Asp Gln Lys Gly Val Arg Val Ala Pro Gly Gln Ser Val Thr Val
```

```
230                 235                 240                 245

ggg atg cag gta agc gtc gaa aag cgt gct tagttttttg ctttgaactc     885
Gly Met Gln Val Ser Val Glu Lys Arg Ala
                250                 255

gcg                                                               888


<210> 2710
<211> 255
<212> PRT
<213> Corynebacterium glutamicum

<400> 2710
Met Thr Thr Phe Ile Thr Ser Gly Gly Leu Glu Ile Ser Pro Ala Gly
  1               5                  10                  15

Ala His Ile Val His Ala Glu Ser Pro Glu Gly Glu Leu Leu Phe Val
            20                  25                  30

Ser Ser Ala Ser Gln Tyr Gly Glu Gly Asn Ala Ile Arg Gly Gly Val
         35                  40                  45

Pro Ile Ile Ala Pro Trp Phe Gly Gly Leu Leu Gly Leu Asp Pro Ala
     50                  55                  60

His Gly Trp Ala Lys Arg Ser Ala Trp Asp Val Thr Glu His Asp Gly
 65                  70                  75                  80

Gln Ile His Ala Glu Tyr Gly Arg Asp Gly Leu Leu Leu Asp Ile Arg
                85                  90                  95

Ala Asn Ser Thr Lys Asn Gly Phe Glu Ile Thr Leu Arg Ala Tyr Asn
            100                 105                 110

Asp Thr Asp Glu Ala Arg Thr Val Gln Leu Ala Phe His Pro Tyr Phe
        115                 120                 125

Lys Val Asp Asp Val Glu Lys Ile Glu Val Arg Gly Leu Asp Gly Val
    130                 135                 140

Asp Ile Leu Asn Arg Leu Asn Asn Glu Val Glu Thr Gln Asp Gly Pro
145                 150                 155                 160

Val Thr Phe Asp Gly Glu Phe Asp Arg Ile Ala Leu Gly Thr Pro Val
                165                 170                 175

Val Arg Ile Phe Asp Thr Asp Arg Ile Ile Thr Ile Glu Gly Asp Gly
            180                 185                 190

His Asp Ser Thr Val Val Trp Asn Pro Gly Glu Ser Arg Ala Ser Thr
        195                 200                 205

Val Ala Asp Ile Gly Glu Gly Glu Trp Arg Asp Phe Val Cys Val Glu
    210                 215                 220

Pro Ala Leu Leu Gly Ala Asp Gln Lys Gly Val Arg Val Ala Pro Gly
225                 230                 235                 240

Gln Ser Val Thr Val Gly Met Gln Val Ser Val Glu Lys Arg Ala
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245 250 255

<210> 2711
<211> 603
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(580)
<223> RXA02412

<400> 2711
tgcggtgcga gcaacttcgg agactattgg ctctcctaca gctgtggcat ccgcgaaacg 60

ttcacccaaa ggcagtctca ttgggttgat cttgatcttg gtg gcc atc atc gtg 115
Val Ala Ile Ile Val
1 5

att gcg ttt gtc ttg ttg ttc aac agc ctc gtt gca cca aat aat tcc 163
Ile Ala Phe Val Leu Leu Phe Asn Ser Leu Val Ala Pro Asn Asn Ser
10 15 20

tcg agc cct gtg gca agt cca agc acc tct gaa tct gtg gag caa act 211
Ser Ser Pro Val Ala Ser Pro Ser Thr Ser Glu Ser Val Glu Gln Thr
25 30 35

att tcg gaa tcc cct gag tca ccg agc gcg aca gag gat cag ccc cca 259
Ile Ser Glu Ser Pro Glu Ser Pro Ser Ala Thr Glu Asp Gln Pro Pro
40 45 50

agc agt gca acg gaa act ccc cga aac cgc cct gcg caa cca tca ctt 307
Ser Ser Ala Thr Glu Thr Pro Arg Asn Arg Pro Ala Gln Pro Ser Leu
55 60 65

cct gcg gga gca tca cca gcc aat gat gct gct gcc acc cag acc gat 355
Pro Ala Gly Ala Ser Pro Ala Asn Asp Ala Ala Ala Thr Gln Thr Asp
70 75 80 85

gcc ggc aat tta aac aat gtg tac acc ggg tca gcg tcc acc tca gca 403
Ala Gly Asn Leu Asn Asn Val Tyr Thr Gly Ser Ala Ser Thr Ser Ala
90 95 100

ggt ttt gct caa gcc gtc cga gat gct ttt gta aac cac tat tta gac 451
Gly Phe Ala Gln Ala Val Arg Asp Ala Phe Val Asn His Tyr Leu Asp
105 110 115

acc aat gaa cta tcc ggc agg gtg aca gcc acc agc cct gtc act ggc 499
Thr Asn Glu Leu Ser Gly Arg Val Thr Ala Thr Ser Pro Val Thr Gly
120 125 130

gga aac tac acc atg aac tgc gaa gac aac ggc gag tac gtc acc tgc 547
Gly Asn Tyr Thr Met Asn Cys Glu Asp Asn Gly Glu Tyr Val Thr Cys
135 140 145

aca ggt ggc aac aac gcc gtt gtc tac att tct taaaacttct aactacaccc 600
Thr Gly Gly Asn Asn Ala Val Val Tyr Ile Ser
150 155 160

ggg 603

<210> 2712
<211> 160
<212> PRT
<213> Corynebacterium glutamicum

<400> 2712

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Val Ala Ile Ile Val Ile Ala Phe Val Leu Leu Phe Asn Ser Leu Val
  1               5                  10                  15

Ala Pro Asn Asn Ser Ser Ser Pro Val Ala Ser Pro Ser Thr Ser Glu
             20                  25                  30

Ser Val Glu Gln Thr Ile Ser Glu Ser Pro Glu Ser Pro Ser Ala Thr
         35                  40                  45

Glu Asp Gln Pro Pro Ser Ser Ala Thr Glu Thr Pro Arg Asn Arg Pro
     50                  55                  60

Ala Gln Pro Ser Leu Pro Ala Gly Ala Ser Pro Ala Asn Asp Ala Ala
 65                  70                  75                  80

Ala Thr Gln Thr Asp Ala Gly Asn Leu Asn Asn Val Tyr Thr Gly Ser
                85                  90                  95

Ala Ser Thr Ser Ala Gly Phe Ala Gln Ala Val Arg Asp Ala Phe Val
            100                 105                 110

Asn His Tyr Leu Asp Thr Asn Glu Leu Ser Gly Arg Val Thr Ala Thr
        115                 120                 125

Ser Pro Val Thr Gly Gly Asn Tyr Thr Met Asn Cys Glu Asp Asn Gly
    130                 135                 140

Glu Tyr Val Thr Cys Thr Gly Gly Asn Asn Ala Val Val Tyr Ile Ser
145                 150                 155                 160
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<210> 2713
<211> 2247
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2224)
<223> RXA02417

<400> 2713

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cgctgttcag aggacttccg cgggggtcga cagtataacg aattagcgtc actagaataa 60

tcgggctgtt tagttcttca caccaacata atcttatgta atg gac atg aac tct   115
                                              Met Asp Met Asn Ser
                                                1               5

tct gac cga ttg gct cta cgc acc gcg tta gag aaa ttg tcg gca tcg   163
Ser Asp Arg Leu Ala Leu Arg Thr Ala Leu Glu Lys Leu Ser Ala Ser
```

```
                  10                  15                  20

gct acc gcc atg gcg tca gcg agc aat gac atc aaa gat ctc gtt gca   211
Ala Thr Ala Met Ala Ser Ala Ser Asn Asp Ile Lys Asp Leu Val Ala
             25                  30                  35

cgc ctt gat gcc caa gag atg tcg ctt atc gac gca aac ccg gct ccc   259
Arg Leu Asp Ala Gln Glu Met Ser Leu Ile Asp Ala Asn Pro Ala Pro
         40                  45                  50

acc cca gcg ccc act gcc cca ccc gag gct cag ctt gag ccc caa cca   307
Thr Pro Ala Pro Thr Ala Pro Pro Glu Ala Gln Leu Glu Pro Gln Pro
     55                  60                  65

ctg gtg tat gca acc gcc tca acg gcg cct gca ctg gcg gat gtt tcc   355
Leu Val Tyr Ala Thr Ala Ser Thr Ala Pro Ala Leu Ala Asp Val Ser
 70                  75                  80                  85

ggg acc aac cgt att cca cgt ttc gtt cgg cat cgc gcc ctg gat cca   403
Gly Thr Asn Arg Ile Pro Arg Phe Val Arg His Arg Ala Leu Asp Pro
                 90                  95                 100

gcg agc gaa ggc tgg cca ctt ggc gtc gag aag caa aaa gtg cag gct   451
Ala Ser Glu Gly Trp Pro Leu Gly Val Glu Lys Gln Lys Val Gln Ala
            105                 110                 115

cct gcg tac ccg cac ccc gtc cgg cca gct cgt ccg gca aag ccg ccg   499
Pro Ala Tyr Pro His Pro Val Arg Pro Ala Arg Pro Ala Lys Pro Pro
        120                 125                 130

atg acg tcg gag gaa aag atc atg cgt ggc gtg gcg atc ggc ggt ggt   547
Met Thr Ser Glu Glu Lys Ile Met Arg Gly Val Ala Ile Gly Gly Gly
    135                 140                 145

gtg atc acc gtg gcc ggc gtg att ttg ctg gtg tcg gtg gcg att caa   595
Val Ile Thr Val Ala Gly Val Ile Leu Leu Val Ser Val Ala Ile Gln
150                 155                 160                 165

cgc ggt tgg ctt ggt ccg ctg ggt cgt gtg att ggt gcg tac ctg ctg   643
Arg Gly Trp Leu Gly Pro Leu Gly Arg Val Ile Gly Ala Tyr Leu Leu
                170                 175                 180

gcg gtg ctg ctt ctt ggc gcc gca cat tat gtg cgc aag cgc gga acc   691
Ala Val Leu Leu Leu Gly Ala Ala His Tyr Val Arg Lys Arg Gly Thr
            185                 190                 195

cgt gtg gaa gca ctc gtt gcg ttg acg gtt acc tcc cag att gcg ttt   739
Arg Val Glu Ala Leu Val Ala Leu Thr Val Thr Ser Gln Ile Ala Phe
        200                 205                 210

ctt gcc aca acg agt gca atc atc ttc att ttg gaa tgg tgg ccg cct   787
Leu Ala Thr Thr Ser Ala Ile Ile Phe Ile Leu Glu Trp Trp Pro Pro
    215                 220                 225

gga ttg ggc tcg ctg gtg gca tta ata ggc aat att ggg ttc tta atc   835
Gly Leu Gly Ser Leu Val Ala Leu Ile Gly Asn Ile Gly Phe Leu Ile
230                 235                 240                 245

gtt ggt cga ttg tgg agc cta tcc aaa acc gag aag tcc gcg gcc gaa   883
Val Gly Arg Leu Trp Ser Leu Ser Lys Thr Glu Lys Ser Ala Ala Glu
                250                 255                 260
```

```
ggc cac aca gta ttt gtg gga gcc atc gcc gtt tca gga ttc tcc gcg   931
Gly His Thr Val Phe Val Gly Ala Ile Ala Val Ser Gly Phe Ser Ala
            265                 270                 275

ata ctc ttc gcg ctc tcc gcc gat gcc tgg tgg cca att ttc tcc att   979
Ile Leu Phe Ala Leu Ser Ala Asp Ala Trp Trp Pro Ile Phe Ser Ile
        280                 285                 290

gtt gcg gca ttg ttg ctg tcg tac cgc atc tcc acg aat atc atc cga   1027
Val Ala Ala Leu Leu Leu Ser Tyr Arg Ile Ser Thr Asn Ile Ile Arg
    295                 300                 305

gcg agc atg gcg gca ttc gcg gtc att ctg cag ttt gtt ttg tcg gca   1075
Ala Ser Met Ala Ala Phe Ala Val Ile Leu Gln Phe Val Leu Ser Ala
310                 315                 320                 325

tcc tgg caa acc atg gaa tgg cca gca aca atc gtc ggc aca att act   1123
Ser Trp Gln Thr Met Glu Trp Pro Ala Thr Ile Val Gly Thr Ile Thr
                330                 335                 340

gca gtc cta ctc gta gcc ttg aca ttg tgg gat ccg ttt aag atc acc   1171
Ala Val Leu Leu Val Ala Leu Thr Leu Trp Asp Pro Phe Lys Ile Thr
            345                 350                 355

gcc acc gac agc cac gac atc gcg ttg gag gaa tac tgg cgc agc ttt   1219
Ala Thr Asp Ser His Asp Ile Ala Leu Glu Glu Tyr Trp Arg Ser Phe
        360                 365                 370

gaa acc aac cct gtt tcc acg tgg gtg ggt gct gtt tct ccg gtg ctc   1267
Glu Thr Asn Pro Val Ser Thr Trp Val Gly Ala Val Ser Pro Val Leu
    375                 380                 385

atc gtg ttc atc acc acc agc atg ttc att gca gtc gac tgg cca tgg   1315
Ile Val Phe Ile Thr Thr Ser Met Phe Ile Ala Val Asp Trp Pro Trp
390                 395                 400                 405

ctt gcc ctg ata cca gcg tgt gcg gtg gca gct ctc gga att ttc gcg   1363
Leu Ala Leu Ile Pro Ala Cys Ala Val Ala Ala Leu Gly Ile Phe Ala
                410                 415                 420

ctg cgc tca tca gac acc gcg tcc att gaa aat caa cgc atg tct cgc   1411
Leu Arg Ser Ser Asp Thr Ala Ser Ile Glu Asn Gln Arg Met Ser Arg
            425                 430                 435

ctc att gct gtt gtt ggc ctt gcg ttg att gct gaa act ttt gtc cag   1459
Leu Ile Ala Val Val Gly Leu Ala Leu Ile Ala Glu Thr Phe Val Gln
        440                 445                 450

ctg ttc tac ggc gat ctc ccc acc aac ccg ctt ctc gtc atg gtg ttc   1507
Leu Phe Tyr Gly Asp Leu Pro Thr Asn Pro Leu Leu Val Met Val Phe
    455                 460                 465

ctc atc gcc gga gct gca cta ttt atg tgg ttg cgg atg ctt cca ccg   1555
Leu Ile Ala Gly Ala Ala Leu Phe Met Trp Leu Arg Met Leu Pro Pro
470                 475                 480                 485

cag cgt caa tta ggt gtc gtc cca tgg gtc gct tgg ctg att gcc gcc   1603
Gln Arg Gln Leu Gly Val Val Pro Trp Val Ala Trp Leu Ile Ala Ala
                490                 495                 500
```

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gtg gcg atg acc ggc gtg cta ctg cgc aat gtc gtt tca att tct cca   1651
Val Ala Met Thr Gly Val Leu Leu Arg Asn Val Val Ser Ile Ser Pro
            505                 510                 515

ctg tgg ctc acc gat acc caa gcg ctc atc caa gca ttg ctg atc ttg   1699
Leu Trp Leu Thr Asp Thr Gln Ala Leu Ile Gln Ala Leu Leu Ile Leu
        520                 525                 530

gtg ttc att gcc gcc aca atc caa gtc cgc cgc agc ttc tac gga cac   1747
Val Phe Ile Ala Ala Thr Ile Gln Val Arg Arg Ser Phe Tyr Gly His
    535                 540                 545

aaa ctg tgg ctg caa att ttg gtc ggc ttg acg ctt ctc acg ctg tcc   1795
Lys Leu Trp Leu Gln Ile Leu Val Gly Leu Thr Leu Leu Thr Leu Ser
550                 555                 560                 565

gca att tcc atc gtg acc atc aca acc ttc atc ggt cgc ctc atc gca   1843
Ala Ile Ser Ile Val Thr Ile Thr Thr Phe Ile Gly Arg Leu Ile Ala
                570                 575                 580

gga aat gcc ggc atg atg ctc gga ttc ctc atc ggc cac gcc acg gtt   1891
Gly Asn Ala Gly Met Met Leu Gly Phe Leu Ile Gly His Ala Thr Val
            585                 590                 595

tct atc ctg tgg atg gtc atc gcc gca gca ctg atg ctt aat agg aag   1939
Ser Ile Leu Trp Met Val Ile Ala Ala Ala Leu Met Leu Asn Arg Lys
        600                 605                 610

ctt ctc gac gcg ccc ggc gcc ctt tgg acc ggc gtt ggc ttg gcg gtt   1987
Leu Leu Asp Ala Pro Gly Ala Leu Trp Thr Gly Val Gly Leu Ala Val
    615                 620                 625

gcg ggc acc ttc aag ctg gtg ttc ttt gac ctg gtc gcg ctg tcc gga   2035
Ala Gly Thr Phe Lys Leu Val Phe Phe Asp Leu Val Ala Leu Ser Gly
630                 635                 640                 645

gtt ccc cgc gca att gcc ttc ctg ctc tcc ggt atc gca ctg ctg aca   2083
Val Pro Arg Ala Ile Ala Phe Leu Leu Ser Gly Ile Ala Leu Leu Thr
                650                 655                 660

atc gct gct atg agg ggc cgg aga acc tca gaa aac aag gcc gac gta   2131
Ile Ala Ala Met Arg Gly Arg Arg Thr Ser Glu Asn Lys Ala Asp Val
            665                 670                 675

gct aga cct cag gtg gct aga cat ggg gcg act agc cat aaa aat gag   2179
Ala Arg Pro Gln Val Ala Arg His Gly Ala Thr Ser His Lys Asn Glu
        680                 685                 690

gag cct tcc cat gaa agc ccc tca tct tct cct aca aca act ctt       2224
Glu Pro Ser His Glu Ser Pro Ser Ser Ser Pro Thr Thr Thr Leu
    695                 700                 705

taaggaattg gccggtgtag gaa                                        2247
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<210> 2714
<211> 708
<212> PRT
<213> Corynebacterium glutamicum

<400> 2714

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Met Asp Met Asn Ser Ser Asp Arg Leu Ala Leu Arg Thr Ala Leu Glu
  1               5                  10                  15

Lys Leu Ser Ala Ser Ala Thr Ala Met Ala Ser Ala Ser Asn Asp Ile
             20                  25                  30

Lys Asp Leu Val Ala Arg Leu Asp Ala Gln Glu Met Ser Leu Ile Asp
         35                  40                  45

Ala Asn Pro Ala Pro Thr Pro Ala Pro Thr Ala Pro Pro Glu Ala Gln
     50                  55                  60

Leu Glu Pro Gln Pro Leu Val Tyr Ala Thr Ala Ser Thr Ala Pro Ala
 65                  70                  75                  80

Leu Ala Asp Val Ser Gly Thr Asn Arg Ile Pro Arg Phe Val Arg His
                 85                  90                  95

Arg Ala Leu Asp Pro Ala Ser Glu Gly Trp Pro Leu Gly Val Glu Lys
            100                 105                 110

Gln Lys Val Gln Ala Pro Ala Tyr Pro His Pro Val Arg Pro Ala Arg
        115                 120                 125

Pro Ala Lys Pro Pro Met Thr Ser Glu Glu Lys Ile Met Arg Gly Val
    130                 135                 140

Ala Ile Gly Gly Gly Val Ile Thr Val Ala Gly Val Ile Leu Leu Val
145                 150                 155                 160

Ser Val Ala Ile Gln Arg Gly Trp Leu Gly Pro Leu Gly Arg Val Ile
                165                 170                 175

Gly Ala Tyr Leu Leu Ala Val Leu Leu Leu Gly Ala Ala His Tyr Val
            180                 185                 190

Arg Lys Arg Gly Thr Arg Val Glu Ala Leu Val Ala Leu Thr Val Thr
        195                 200                 205

Ser Gln Ile Ala Phe Leu Ala Thr Thr Ser Ala Ile Ile Phe Ile Leu
    210                 215                 220

Glu Trp Trp Pro Pro Gly Leu Gly Ser Leu Val Ala Leu Ile Gly Asn
225                 230                 235                 240

Ile Gly Phe Leu Ile Val Gly Arg Leu Trp Ser Leu Ser Lys Thr Glu
                245                 250                 255

Lys Ser Ala Ala Glu Gly His Thr Val Phe Val Gly Ala Ile Ala Val
            260                 265                 270

Ser Gly Phe Ser Ala Ile Leu Phe Ala Leu Ser Ala Asp Ala Trp Trp
        275                 280                 285

Pro Ile Phe Ser Ile Val Ala Ala Leu Leu Leu Ser Tyr Arg Ile Ser
    290                 295                 300

Thr Asn Ile Ile Arg Ala Ser Met Ala Ala Phe Ala Val Ile Leu Gln
305                 310                 315                 320

Phe Val Leu Ser Ala Ser Trp Gln Thr Met Glu Trp Pro Ala Thr Ile
```

```
                325                 330                 335

Val Gly Thr Ile Thr Ala Val Leu Leu Val Ala Leu Thr Leu Trp Asp
            340                 345                 350

Pro Phe Lys Ile Thr Ala Thr Asp Ser His Asp Ile Ala Leu Glu Glu
        355                 360                 365

Tyr Trp Arg Ser Phe Glu Thr Asn Pro Val Ser Thr Trp Val Gly Ala
    370                 375                 380

Val Ser Pro Val Leu Ile Val Phe Ile Thr Thr Ser Met Phe Ile Ala
385                 390                 395                 400

Val Asp Trp Pro Trp Leu Ala Leu Ile Pro Ala Cys Ala Val Ala Ala
                405                 410                 415

Leu Gly Ile Phe Ala Leu Arg Ser Ser Asp Thr Ala Ser Ile Glu Asn
            420                 425                 430

Gln Arg Met Ser Arg Leu Ile Ala Val Val Gly Leu Ala Leu Ile Ala
        435                 440                 445

Glu Thr Phe Val Gln Leu Phe Tyr Gly Asp Leu Pro Thr Asn Pro Leu
    450                 455                 460

Leu Val Met Val Phe Leu Ile Ala Gly Ala Ala Leu Phe Met Trp Leu
465                 470                 475                 480

Arg Met Leu Pro Pro Gln Arg Gln Leu Gly Val Val Pro Trp Val Ala
                485                 490                 495

Trp Leu Ile Ala Ala Val Ala Met Thr Gly Val Leu Leu Arg Asn Val
            500                 505                 510

Val Ser Ile Ser Pro Leu Trp Leu Thr Asp Thr Gln Ala Leu Ile Gln
        515                 520                 525

Ala Leu Leu Ile Leu Val Phe Ile Ala Ala Thr Ile Gln Val Arg Arg
    530                 535                 540

Ser Phe Tyr Gly His Lys Leu Trp Leu Gln Ile Leu Val Gly Leu Thr
545                 550                 555                 560

Leu Leu Thr Leu Ser Ala Ile Ser Ile Val Thr Ile Thr Thr Phe Ile
                565                 570                 575

Gly Arg Leu Ile Ala Gly Asn Ala Gly Met Met Leu Gly Phe Leu Ile
            580                 585                 590

Gly His Ala Thr Val Ser Ile Leu Trp Met Val Ile Ala Ala Ala Leu
        595                 600                 605

Met Leu Asn Arg Lys Leu Leu Asp Ala Pro Gly Ala Leu Trp Thr Gly
    610                 615                 620

Val Gly Leu Ala Val Ala Gly Thr Phe Lys Leu Val Phe Phe Asp Leu
625                 630                 635                 640

Val Ala Leu Ser Gly Val Pro Arg Ala Ile Ala Phe Leu Leu Ser Gly
                645                 650                 655
```

```
Ile Ala Leu Leu Thr Ile Ala Ala Met Arg Gly Arg Arg Thr Ser Glu
            660                 665                 670

Asn Lys Ala Asp Val Ala Arg Pro Gln Val Ala Arg His Gly Ala Thr
        675                 680                 685

Ser His Lys Asn Glu Glu Pro Ser His Glu Ser Pro Ser Ser Ser Pro
    690                 695                 700

Thr Thr Thr Leu
705
```

<210> 2715
<211> 933
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(910)
<223> RXA02421

<400> 2715

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cggtgtactt tagcaacaag gaaaaataac tatctacggc ctgttaatag ttcaacctac 60

aggccaaacc cgccttcatt aatgaattgt gagatcgacc atg aca ttg ctc ttg   115
                                          Met Thr Leu Leu Leu
                                            1               5

aag cca att ttg cag gct gcg gga atc aat cct gaa gat gcg tta gca   163
Lys Pro Ile Leu Gln Ala Ala Gly Ile Asn Pro Glu Asp Ala Leu Ala
                10                  15                  20

atg cgt cat gta ttt att tcg atc cac gag gac acc aat tcc aat ggt   211
Met Arg His Val Phe Ile Ser Ile His Glu Asp Thr Asn Ser Asn Gly
            25                  30                  35

att acc cgt gaa tct aaa gac gaa gag att ctc gcc tac aca gct agc   259
Ile Thr Arg Glu Ser Lys Asp Glu Glu Ile Leu Ala Tyr Thr Ala Ser
        40                  45                  50

cag tca agt gat ccg cgt aga ttc cca ctg aat ccg cca cgc ttt tgg   307
Gln Ser Ser Asp Pro Arg Arg Phe Pro Leu Asn Pro Pro Arg Phe Trp
    55                  60                  65

atg gtg ttc atc cga gaa ggt ggc tcg cag gct cga cta tgg aaa gtg   355
Met Val Phe Ile Arg Glu Gly Gly Ser Gln Ala Arg Leu Trp Lys Val
70                  75                  80                  85

gtg gaa aac cac ggc gaa gtc acc aat gat ggc gta cgc aga gtc ttc   403
Val Glu Asn His Gly Glu Val Thr Asn Asp Gly Val Arg Arg Val Phe
                90                  95                  100

aac ctt act gag att gaa ctc atg gat gac ctt gca ggc aga ctc gtt   451
Asn Leu Thr Glu Ile Glu Leu Met Asp Asp Leu Ala Gly Arg Leu Val
            105                 110                 115

att cgt tgg aat tca cca cgc aag tgg tgg att aag ggc act act gct   499
Ile Arg Trp Asn Ser Pro Arg Lys Trp Trp Ile Lys Gly Thr Thr Ala
```

```
        120                 125                 130

gcc cta tac acc gtg gat act att gcc gat gcg gag cct att ccg ttt   547
Ala Leu Tyr Thr Val Asp Thr Ile Ala Asp Ala Glu Pro Ile Pro Phe
    135                 140                 145

cca ggt ttc gac aat ctt gtc ctg agc tac cca ttt ctt caa gaa gtg   595
Pro Gly Phe Asp Asn Leu Val Leu Ser Tyr Pro Phe Leu Gln Glu Val
150                 155                 160                 165

atg cgt gaa cct gcc tat gct tcg tgg cgc aca gct ctt ggt gct gtc   643
Met Arg Glu Pro Ala Tyr Ala Ser Trp Arg Thr Ala Leu Gly Ala Val
                170                 175                 180

aaa ggt att tac ctc att acc gat acc cgt act ggc cgc cac tat gtc   691
Lys Gly Ile Tyr Leu Ile Thr Asp Thr Arg Thr Gly Arg His Tyr Val
            185                 190                 195

ggc aaa gct gaa gga cta gaa aac ata cgc caa cgc tgg aac agc tac   739
Gly Lys Ala Glu Gly Leu Glu Asn Ile Arg Gln Arg Trp Asn Ser Tyr
        200                 205                 210

gcc acc aat gga cat ggc gga aac gta aaa ctc aaa cag ctt aag ccc   787
Ala Thr Asn Gly His Gly Gly Asn Val Lys Leu Lys Gln Leu Lys Pro
    215                 220                 225

gac aca ttt cgt ttt tcg ttg ctt cgg gtc ttt gat ccc gca act cca   835
Asp Thr Phe Arg Phe Ser Leu Leu Arg Val Phe Asp Pro Ala Thr Pro
230                 235                 240                 245

act agc att att aac gct gct gaa agc cac ttt aaa att gct ctc gac   883
Thr Ser Ile Ile Asn Ala Ala Glu Ser His Phe Lys Ile Ala Leu Asp
                250                 255                 260

acg atc aag cac gga tta aac gca aac taatcgcagc tccccaaccc         930
Thr Ile Lys His Gly Leu Asn Ala Asn
            265                 270

caa                                                              933
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<210> 2716
<211> 270
<212> PRT
<213> Corynebacterium glutamicum

<400> 2716

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Met Thr Leu Leu Leu Lys Pro Ile Leu Gln Ala Ala Gly Ile Asn Pro
  1               5                  10                  15

Glu Asp Ala Leu Ala Met Arg His Val Phe Ile Ser Ile His Glu Asp
             20                  25                  30

Thr Asn Ser Asn Gly Ile Thr Arg Glu Ser Lys Asp Glu Glu Ile Leu
         35                  40                  45

Ala Tyr Thr Ala Ser Gln Ser Ser Asp Pro Arg Arg Phe Pro Leu Asn
     50                  55                  60

Pro Pro Arg Phe Trp Met Val Phe Ile Arg Glu Gly Gly Ser Gln Ala
 65                  70                  75                  80
```

```
Arg Leu Trp Lys Val Val Glu Asn His Gly Glu Val Thr Asn Asp Gly
                85                  90                  95

Val Arg Arg Val Phe Asn Leu Thr Glu Ile Glu Leu Met Asp Asp Leu
            100                 105                 110

Ala Gly Arg Leu Val Ile Arg Trp Asn Ser Pro Arg Lys Trp Trp Ile
        115                 120                 125

Lys Gly Thr Thr Ala Ala Leu Tyr Thr Val Asp Thr Ile Ala Asp Ala
    130                 135                 140

Glu Pro Ile Pro Phe Pro Gly Phe Asp Asn Leu Val Leu Ser Tyr Pro
145                 150                 155                 160

Phe Leu Gln Glu Val Met Arg Glu Pro Ala Tyr Ala Ser Trp Arg Thr
                165                 170                 175

Ala Leu Gly Ala Val Lys Gly Ile Tyr Leu Ile Thr Asp Thr Arg Thr
            180                 185                 190

Gly Arg His Tyr Val Gly Lys Ala Glu Gly Leu Glu Asn Ile Arg Gln
        195                 200                 205

Arg Trp Asn Ser Tyr Ala Thr Asn Gly His Gly Gly Asn Val Lys Leu
    210                 215                 220

Lys Gln Leu Lys Pro Asp Thr Phe Arg Phe Ser Leu Leu Arg Val Phe
225                 230                 235                 240

Asp Pro Ala Thr Pro Thr Ser Ile Ile Asn Ala Ala Glu Ser His Phe
                245                 250                 255

Lys Ile Ala Leu Asp Thr Ile Lys His Gly Leu Asn Ala Asn
            260                 265                 270


<210> 2717
<211> 653
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(630)
<223> RXA02425

<400> 2717
ccc ggc gcc ttt gat gaa tta acc agt gtt tgg gga gaa aaa ggc gga   48
Pro Gly Ala Phe Asp Glu Leu Thr Ser Val Trp Gly Glu Lys Gly Gly
  1               5                  10                  15

agt tgg gcc gct gtt atc ggc ttc ttc ggt ggc atc gcg ctg atc gcc   96
Ser Trp Ala Ala Val Ile Gly Phe Phe Gly Gly Ile Ala Leu Ile Ala
             20                  25                  30

atc atc gac cgc tta gtc ccc acg gcg att aac ccc cac gag ccc tcc   144
Ile Ile Asp Arg Leu Val Pro Thr Ala Ile Asn Pro His Glu Pro Ser
         35                  40                  45
```

```
acc gtg gga ggc gcc gtt gaa gga ttc gag cgc cgc aac cgc atg atg   192
Thr Val Gly Gly Ala Val Glu Gly Phe Glu Arg Arg Asn Arg Met Met
     50                  55                  60

aaa atg ggt gtg ctc act gcg ctg gcc atc gcg atc cac aac ttt ccc   240
Lys Met Gly Val Leu Thr Ala Leu Ala Ile Ala Ile His Asn Phe Pro
 65                  70                  75                  80

gaa ggt ttc gct aca ttc ttg gcc gga ttg tcc gat cca atg atc gcg   288
Glu Gly Phe Ala Thr Phe Leu Ala Gly Leu Ser Asp Pro Met Ile Ala
                85                  90                  95

atc cct gtg gcc gtg gca att gcc att cac aat att cca gag ggc att   336
Ile Pro Val Ala Val Ala Ile Ala Ile His Asn Ile Pro Glu Gly Ile
            100                 105                 110

gcg gtg ccg gtg cca ctg agg gaa gct aca ggg tca cgt cga aaa gca   384
Ala Val Pro Val Pro Leu Arg Glu Ala Thr Gly Ser Arg Arg Lys Ala
        115                 120                 125

tta ggt tgg gcg acc ctc tcc ggc ctt gct gag ccc gcc ggc gcc ctc   432
Leu Gly Trp Ala Thr Leu Ser Gly Leu Ala Glu Pro Ala Gly Ala Leu
    130                 135                 140

atc gga ttc ctg ctg ctc atg ccc ttt atc gga cca gaa gca ctc ggc   480
Ile Gly Phe Leu Leu Leu Met Pro Phe Ile Gly Pro Glu Ala Leu Gly
145                 150                 155                 160

ctg tgc ttc gcc gca gtt gcc ggc gtg atg gtg ttc atc agc gtc gat   528
Leu Cys Phe Ala Ala Val Ala Gly Val Met Val Phe Ile Ser Val Asp
                165                 170                 175

gaa cta ctg ccc act gcc atc tcc agc ggc aaa cac cac acc gcc atc   576
Glu Leu Leu Pro Thr Ala Ile Ser Ser Gly Lys His His Thr Ala Ile
            180                 185                 190

tac gga ctc atc gct ggc atg gca gtc atg gcg atc agc ctg ctg ctg   624
Tyr Gly Leu Ile Ala Gly Met Ala Val Met Ala Ile Ser Leu Leu Leu
        195                 200                 205

ttt atc tagcgttcag ccgcaacaag cat                                 653
Phe Ile
    210


<210> 2718
<211> 210
<212> PRT
<213> Corynebacterium glutamicum

<400> 2718
Pro Gly Ala Phe Asp Glu Leu Thr Ser Val Trp Gly Glu Lys Gly Gly
  1               5                  10                  15

Ser Trp Ala Ala Val Ile Gly Phe Phe Gly Gly Ile Ala Leu Ile Ala
             20                  25                  30

Ile Ile Asp Arg Leu Val Pro Thr Ala Ile Asn Pro His Glu Pro Ser
         35                  40                  45

Thr Val Gly Gly Ala Val Glu Gly Phe Glu Arg Arg Asn Arg Met Met
```

```
     50                  55                  60

Lys Met Gly Val Leu Thr Ala Leu Ala Ile Ala Ile His Asn Phe Pro
 65                  70                  75                  80

Glu Gly Phe Ala Thr Phe Leu Ala Gly Leu Ser Asp Pro Met Ile Ala
                85                  90                  95

Ile Pro Val Ala Val Ala Ile Ala Ile His Asn Ile Pro Glu Gly Ile
            100                 105                 110

Ala Val Pro Val Pro Leu Arg Glu Ala Thr Gly Ser Arg Arg Lys Ala
        115                 120                 125

Leu Gly Trp Ala Thr Leu Ser Gly Leu Ala Glu Pro Ala Gly Ala Leu
    130                 135                 140

Ile Gly Phe Leu Leu Leu Met Pro Phe Ile Gly Pro Glu Ala Leu Gly
145                 150                 155                 160

Leu Cys Phe Ala Ala Val Ala Gly Val Met Val Phe Ile Ser Val Asp
                165                 170                 175

Glu Leu Leu Pro Thr Ala Ile Ser Ser Gly Lys His His Thr Ala Ile
            180                 185                 190

Tyr Gly Leu Ile Ala Gly Met Ala Val Met Ala Ile Ser Leu Leu Leu
        195                 200                 205

Phe Ile
    210


<210> 2719
<211> 510
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(487)
<223> RXA02427

<400> 2719
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ctcgcgcagg gaatcgtcat cgacgacgag gtgaactagc gtg gat ttt gag ttg   115
                                            Val Asp Phe Glu Leu
                                              1               5

ggt aaa cgc tgc ccc tgc gga act ggc ctt acc tac ggt gag tgc tgc   163
Gly Lys Arg Cys Pro Cys Gly Thr Gly Leu Thr Tyr Gly Glu Cys Cys
                10                  15                  20

tac cgc ttt cac tcc ggc gaa tgg gtg gcc ccc acc gct gaa gcg ctc   211
Tyr Arg Phe His Ser Gly Glu Trp Val Ala Pro Thr Ala Glu Ala Leu
            25                  30                  35

atg cga tct cgg ttc acc gcc ttt gct gtt gga aat tcc cag tac ctt   259
Met Arg Ser Arg Phe Thr Ala Phe Ala Val Gly Asn Ser Gln Tyr Leu
        40                  45                  50
```

```
ctt gac act tgg gat cca gaa acc cgg cca agc gaa ctc ggc ctc gat   307
Leu Asp Thr Trp Asp Pro Glu Thr Arg Pro Ser Glu Leu Gly Leu Asp
     55                  60                  65

atg gga att gat ttc tac cgc ctc gac atc ctc gag acc acc ggc ggt   355
Met Gly Ile Asp Phe Tyr Arg Leu Asp Ile Leu Glu Thr Thr Gly Gly
 70                  75                  80                  85

gga ccc ttc gat tcc acc ggc acc gta aaa ttc caa gcc ttc tac aag   403
Gly Pro Phe Asp Ser Thr Gly Thr Val Lys Phe Gln Ala Phe Tyr Lys
                90                  95                 100

ggg ctc gcc tcc ggc gtc caa gaa gaa gac tcc aca ttc cgc aag gtc   451
Gly Leu Ala Ser Gly Val Gln Glu Glu Asp Ser Thr Phe Arg Lys Val
            105                 110                 115

aac ggc gcg tgg gtc tat tcc aca gga gat gtc gac tagtttcccc        497
Asn Gly Ala Trp Val Tyr Ser Thr Gly Asp Val Asp
        120                 125

acacgtgcaa tag                                                   510
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Sequence Listing

<210> 2720
<211> 129
<212> PRT
<213> Corynebacterium glutamicum

<400> 2720

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Val Asp Phe Glu Leu Gly Lys Arg Cys Pro Cys Gly Thr Gly Leu Thr
  1               5                  10                  15

Tyr Gly Glu Cys Cys Tyr Arg Phe His Ser Gly Glu Trp Val Ala Pro
             20                  25                  30

Thr Ala Glu Ala Leu Met Arg Ser Arg Phe Thr Ala Phe Ala Val Gly
         35                  40                  45

Asn Ser Gln Tyr Leu Leu Asp Thr Trp Asp Pro Glu Thr Arg Pro Ser
     50                  55                  60

Glu Leu Gly Leu Asp Met Gly Ile Asp Phe Tyr Arg Leu Asp Ile Leu
 65                  70                  75                  80

Glu Thr Thr Gly Gly Gly Pro Phe Asp Ser Thr Gly Thr Val Lys Phe
                 85                  90                  95

Gln Ala Phe Tyr Lys Gly Leu Ala Ser Gly Val Gln Glu Glu Asp Ser
            100                 105                 110

Thr Phe Arg Lys Val Asn Gly Ala Trp Val Tyr Ser Thr Gly Asp Val
        115                 120                 125

Asp
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<210> 2721
<211> 309
<212> DNA

<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(286)
<223> RXA02430

<400> 2721
cttgtagtca agcgtggacc aaatgcaggc gctcgattcc ttctggacca gccaaccacg 60

accgctggtc gtcacccaga aagtgacatc ttccttgatg atg tca ccc gtt tca 115
Met Ser Pro Val Ser
1 5

cgt cgc cac gca gag ttc cgc atc aat gaa ggt gaa ttt gaa gtc gtg 163
Arg Arg His Ala Glu Phe Arg Ile Asn Glu Gly Glu Phe Glu Val Val
10 15 20

gac gta ggg tcc ctc aac gga acc tac gtt aac cgc gag cca cgc aac 211
Asp Val Gly Ser Leu Asn Gly Thr Tyr Val Asn Arg Glu Pro Arg Asn
25 30 35

gct cag gtc atg cag acc ggt gat gag atc cag att ggc aag ttc cgc 259
Ala Gln Val Met Gln Thr Gly Asp Glu Ile Gln Ile Gly Lys Phe Arg
40 45 50

ctg gtt ttc ctc gca ggc cct gct gag taaaaacact tcctaggaaa 306
Leu Val Phe Leu Ala Gly Pro Ala Glu
55 60

gtt 309

<210> 2722
<211> 62
<212> PRT
<213> Corynebacterium glutamicum

<400> 2722
Met Ser Pro Val Ser Arg Arg His Ala Glu Phe Arg Ile Asn Glu Gly
1 5 10 15

Glu Phe Glu Val Val Asp Val Gly Ser Leu Asn Gly Thr Tyr Val Asn
20 25 30

Arg Glu Pro Arg Asn Ala Gln Val Met Gln Thr Gly Asp Glu Ile Gln
35 40 45

Ile Gly Lys Phe Arg Leu Val Phe Leu Ala Gly Pro Ala Glu
50 55 60

<210> 2723
<211> 723
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(700)
<223> RXA02433

<400> 2723
aggcacgaga tcatccatcg tcggttccat agaatgggta gctgtcgaat gctgatagat 60

atttggtgac cagagattag agcaaaggat cattttcatc gtg aag ctt ttc aag 115
Val Lys Leu Phe Lys
1 5

gca acc gca gtt act ttt act gtt gca gca gca ttg gcg ctc agc gcg 163
Ala Thr Ala Val Thr Phe Thr Val Ala Ala Ala Leu Ala Leu Ser Ala
10 15 20

tgc tcc agc agt gat gat tcc tct tcg gag tca agc acc tct tct tcc 211
Cys Ser Ser Ser Asp Asp Ser Ser Ser Glu Ser Ser Thr Ser Ser Ser
25 30 35

acc tct tcg gct gcg tct gat gct gcg act cag tac cca act gct gag 259
Thr Ser Ser Ala Ala Ser Asp Ala Ala Thr Gln Tyr Pro Thr Ala Glu
40 45 50

gaa ctg aat gca att ttg gct gtg gca acc gac cct gag gca cca atc 307
Glu Leu Asn Ala Ile Leu Ala Val Ala Thr Asp Pro Glu Ala Pro Ile
55 60 65

gag gag aag gtg aag act gtt cag ggt tct gag aac gct cct gag ctg 355
Glu Glu Lys Val Lys Thr Val Gln Gly Ser Glu Asn Ala Pro Glu Leu
70 75 80 85

ttt gag acc atg act cag gca aag gtg gag tcg ggt gct gag ttc cag 403
Phe Glu Thr Met Thr Gln Ala Lys Val Glu Ser Gly Ala Glu Phe Gln
90 95 100

gtt gtt ggt tct gtg ctt cct ggc tat gac cca acc tct gag gtt ctg 451
Val Val Gly Ser Val Leu Pro Gly Tyr Asp Pro Thr Ser Glu Val Leu
105 110 115

acc acc gtc atg ttc cag ctt ccg gac cgc gct gag cag gaa gct gaa 499
Thr Thr Val Met Phe Gln Leu Pro Asp Arg Ala Glu Gln Glu Ala Glu
120 125 130

ggc gtg gag ttt gtg aac act gat ggt aat tgg cag ctg tcc cag gat 547
Gly Val Glu Phe Val Asn Thr Asp Gly Asn Trp Gln Leu Ser Gln Asp
135 140 145

tgg gct tgt atc ttg atc acc aat act gtt gct cct gag cag gtt cct 595
Trp Ala Cys Ile Leu Ile Thr Asn Thr Val Ala Pro Glu Gln Val Pro
150 155 160 165

gca atg tgt gtt gga act gat gct tct tcc gct ggt att gaa gag gcc 643
Ala Met Cys Val Gly Thr Asp Ala Ser Ser Ala Gly Ile Glu Glu Ala
170 175 180

cca gct gaa gag ggt gct gtt gtt gag gaa gcc cct gtt gaa gag gtt 691
Pro Ala Glu Glu Gly Ala Val Val Glu Glu Ala Pro Val Glu Glu Val
185 190 195

cct gtt cag tagggtttaa cggctcaggc tga 723
Pro Val Gln
200

<210> 2724
<211> 200
<212> PRT
<213> Corynebacterium glutamicum

<400> 2724
Val Lys Leu Phe Lys Ala Thr Ala Val Thr Phe Thr Val Ala Ala Ala
1 5 10 15

Leu Ala Leu Ser Ala Cys Ser Ser Ser Asp Asp Ser Ser Ser Glu Ser
20 25 30

Ser Thr Ser Ser Ser Thr Ser Ser Ala Ala Ser Asp Ala Ala Thr Gln
35 40 45

Tyr Pro Thr Ala Glu Glu Leu Asn Ala Ile Leu Ala Val Ala Thr Asp
50 55 60

Pro Glu Ala Pro Ile Glu Glu Lys Val Lys Thr Val Gln Gly Ser Glu
65 70 75 80

Asn Ala Pro Glu Leu Phe Glu Thr Met Thr Gln Ala Lys Val Glu Ser
85 90 95

Gly Ala Glu Phe Gln Val Val Gly Ser Val Leu Pro Gly Tyr Asp Pro
100 105 110

Thr Ser Glu Val Leu Thr Thr Val Met Phe Gln Leu Pro Asp Arg Ala
115 120 125

Glu Gln Glu Ala Glu Gly Val Glu Phe Val Asn Thr Asp Gly Asn Trp
130 135 140

Gln Leu Ser Gln Asp Trp Ala Cys Ile Leu Ile Thr Asn Thr Val Ala
145 150 155 160

Pro Glu Gln Val Pro Ala Met Cys Val Gly Thr Asp Ala Ser Ser Ala
165 170 175

Gly Ile Glu Glu Ala Pro Ala Glu Glu Gly Ala Val Val Glu Glu Ala
180 185 190

Pro Val Glu Glu Val Pro Val Gln
195 200

<210> 2725
<211> 933
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(910)
<223> RXA02437

<400> 2725
gcccatcata actacatcga gcgaaatgcc aaccacatgt cccatgcttt tactaatgtg 60

gggtcttaga agaacgcgac caatttaagg agagttgaat atg agc acg att ggc 115
Met Ser Thr Ile Gly

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                                                    1               5

aac ctc aag tta gta gtg gat ggc gca cgt aaa gct tat gga act tat   163
Asn Leu Lys Leu Val Val Asp Gly Ala Arg Lys Ala Tyr Gly Thr Tyr
                10                  15                  20

gcg gat tac cgc gac cgc aag gtg tct gag act tat gat gcg ttg tcc   211
Ala Asp Tyr Arg Asp Arg Lys Val Ser Glu Thr Tyr Asp Ala Leu Ser
            25                  30                  35

caa gct gct ggt gaa tat gca cca aaa gct gag cag gct gta gag act   259
Gln Ala Ala Gly Glu Tyr Ala Pro Lys Ala Glu Gln Ala Val Glu Thr
        40                  45                  50

gcg cgg gaa tca gcg aag gaa ttt tat act gag tcg cgc gat aag gct   307
Ala Arg Glu Ser Ala Lys Glu Phe Tyr Thr Glu Ser Arg Asp Lys Ala
    55                  60                  65

gga aat gtc acc aag gct gct cgt gct cgt ctg gaa aag gcg ctc gct   355
Gly Asn Val Thr Lys Ala Ala Arg Ala Arg Leu Glu Lys Ala Leu Ala
70                  75                  80                  85

gag gct gac aag cag ggc act tct gcg ttg aag gac gca cgt gaa tcg   403
Glu Ala Asp Lys Gln Gly Thr Ser Ala Leu Lys Asp Ala Arg Glu Ser
                90                  95                  100

ggc aag aaa ttg aac cgg aag gcg cgt cga aaa gca gac aag gcc gct   451
Gly Lys Lys Leu Asn Arg Lys Ala Arg Arg Lys Ala Asp Lys Ala Ala
            105                 110                 115

aag gca gcc cgc aag gcg act gaa aag aag gag tcg cac tgg gtg cgc   499
Lys Ala Ala Arg Lys Ala Thr Glu Lys Lys Glu Ser His Trp Val Arg
        120                 125                 130

aat ctg tcg ttg gcg gcg cta gcg acc tcc ggc atc gtc gcg gtg gcc   547
Asn Leu Ser Leu Ala Ala Leu Ala Thr Ser Gly Ile Val Ala Val Ala
    135                 140                 145

tac gcg ttt ttg aac aag acc aag aag gaa acc cca ggc acc cag cct   595
Tyr Ala Phe Leu Asn Lys Thr Lys Lys Glu Thr Pro Gly Thr Gln Pro
150                 155                 160                 165

cca cgg gtt gag gtt cag ttg aag aag gcc gtg gag cag gat gag cct   643
Pro Arg Val Glu Val Gln Leu Lys Lys Ala Val Glu Gln Asp Glu Pro
                170                 175                 180

gag gtt gtg gct gag gct gct gtg gag gag cca gag ttg gtg tac tcc   691
Glu Val Val Ala Glu Ala Ala Val Glu Glu Pro Glu Leu Val Tyr Ser
            185                 190                 195

aca gaa agc cca gaa acc act gaa gcc cca gct gag gcc acc gaa act   739
Thr Glu Ser Pro Glu Thr Thr Glu Ala Pro Ala Glu Ala Thr Glu Thr
        200                 205                 210

cca gca gaa acc acc gaa gaa gaa gcc aaa acc gaa gct gaa cta gag   787
Pro Ala Glu Thr Thr Glu Glu Glu Ala Lys Thr Glu Ala Glu Leu Glu
    215                 220                 225

gca gag ctc gag gct gag gcc gat gcg gag cag gaa gcg gca gaa gag   835
Ala Glu Leu Glu Ala Glu Ala Asp Ala Glu Gln Glu Ala Ala Glu Glu
230                 235                 240                 245
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```
gcg gaa gct gag gcc att cag gct gag ttt gat aag aag aat gca cct   883
Ala Glu Ala Glu Ala Ile Gln Ala Glu Phe Asp Lys Lys Asn Ala Pro
                250                 255                 260

cag cgc acc cag agc gaa aag aag aag taggttaacg cttcaattcg         930
Gln Arg Thr Gln Ser Glu Lys Lys Lys
            265                 270

tgg                                                               933


<210> 2726
<211> 270
<212> PRT
<213> Corynebacterium glutamicum

<400> 2726
Met Ser Thr Ile Gly Asn Leu Lys Leu Val Val Asp Gly Ala Arg Lys
  1               5                  10                  15

Ala Tyr Gly Thr Tyr Ala Asp Tyr Arg Asp Arg Lys Val Ser Glu Thr
             20                  25                  30

Tyr Asp Ala Leu Ser Gln Ala Ala Gly Glu Tyr Ala Pro Lys Ala Glu
         35                  40                  45

Gln Ala Val Glu Thr Ala Arg Glu Ser Ala Lys Glu Phe Tyr Thr Glu
     50                  55                  60

Ser Arg Asp Lys Ala Gly Asn Val Thr Lys Ala Ala Arg Ala Arg Leu
 65                  70                  75                  80

Glu Lys Ala Leu Ala Glu Ala Asp Lys Gln Gly Thr Ser Ala Leu Lys
                 85                  90                  95

Asp Ala Arg Glu Ser Gly Lys Lys Leu Asn Arg Lys Ala Arg Arg Lys
            100                 105                 110

Ala Asp Lys Ala Ala Lys Ala Ala Arg Lys Ala Thr Glu Lys Lys Glu
        115                 120                 125

Ser His Trp Val Arg Asn Leu Ser Leu Ala Ala Leu Ala Thr Ser Gly
    130                 135                 140

Ile Val Ala Val Ala Tyr Ala Phe Leu Asn Lys Thr Lys Lys Glu Thr
145                 150                 155                 160

Pro Gly Thr Gln Pro Pro Arg Val Glu Val Gln Leu Lys Lys Ala Val
                165                 170                 175

Glu Gln Asp Glu Pro Glu Val Val Ala Glu Ala Ala Val Glu Glu Pro
            180                 185                 190

Glu Leu Val Tyr Ser Thr Glu Ser Pro Glu Thr Thr Glu Ala Pro Ala
        195                 200                 205

Glu Ala Thr Glu Thr Pro Ala Glu Thr Thr Glu Glu Glu Ala Lys Thr
    210                 215                 220

Glu Ala Glu Leu Glu Ala Glu Leu Glu Ala Glu Ala Asp Ala Glu Gln
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225                 230                 235                 240

Glu Ala Ala Glu Glu Ala Glu Ala Glu Ala Ile Gln Ala Glu Phe Asp
                245                 250                 255

Lys Lys Asn Ala Pro Gln Arg Thr Gln Ser Glu Lys Lys Lys
            260                 265                 270


<210> 2727
<211> 1077
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1054)
<223> RXA02443

<400> 2727
caagcactgc cgcgggagcc actatcactt tgttaagtgc tgcgatattt tttgccacct 60

tattgacaaa gagtgccatt agtaggttaa acttcaccgc gtg ata ctg aaa gac   115
                                            Val Ile Leu Lys Asp
                                              1               5

att ttc aat aat ggg gag ctc ttt ggg gct tcc tcc gcg aaa aat ttc   163
Ile Phe Asn Asn Gly Glu Leu Phe Gly Ala Ser Ser Ala Lys Asn Phe
                10                  15                  20

cga aaa cta cta gct gtt cca gcc gtt gcc gcc tca cta gct ttt ggt   211
Arg Lys Leu Leu Ala Val Pro Ala Val Ala Ala Ser Leu Ala Phe Gly
            25                  30                  35

atc acc gcc tgt tcc gct gta gat gac acc cct gac att gtg gtc acc   259
Ile Thr Ala Cys Ser Ala Val Asp Asp Thr Pro Asp Ile Val Val Thr
        40                  45                  50

acc aac atc ctg ggt gat gtt gta agc cat atc gtg gga gat tcc gca   307
Thr Asn Ile Leu Gly Asp Val Val Ser His Ile Val Gly Asp Ser Ala
    55                  60                  65

gat gtc caa gta ctc atg aaa ccc aac gca gat cca cat tcc ttc gga   355
Asp Val Gln Val Leu Met Lys Pro Asn Ala Asp Pro His Ser Phe Gly
70                  75                  80                  85

gtc tca gca caa gac gcc gct gcc atg gaa cat gcc gat ctc atc gtg   403
Val Ser Ala Gln Asp Ala Ala Ala Met Glu His Ala Asp Leu Ile Val
                90                  95                  100

gcc aat gga cta gga ctt gaa gag ggc ctt caa tcc aat gtg gac aat   451
Ala Asn Gly Leu Gly Leu Glu Glu Gly Leu Gln Ser Asn Val Asp Asn
            105                 110                 115

gcc aaa agc caa ggg gtt ccc gtc ttg gaa gtc ggc gaa cac atc gat   499
Ala Lys Ser Gln Gly Val Pro Val Leu Glu Val Gly Glu His Ile Asp
        120                 125                 130

gtc att gac tac tcc ccc ggc gtt cca gat cct cac ttt tgg aca gac   547
Val Ile Asp Tyr Ser Pro Gly Val Pro Asp Pro His Phe Trp Thr Asp
    135                 140                 145
```

```
ccg gcg cgc atg atc gcc gcc acg gaa gtt ata gaa gct gaa ctg atc   595
Pro Ala Arg Met Ile Ala Ala Thr Glu Val Ile Glu Ala Glu Leu Ile
150                 155                 160                 165

aaa gaa ctc gat cct tcc ctg act gaa tcg atc aca caa tca gcc cag   643
Lys Glu Leu Asp Pro Ser Leu Thr Glu Ser Ile Thr Gln Ser Ala Gln
                170                 175                 180

cac tac cgt gag gaa ctt gtt gcc ctt gat gag gaa gtc acc gaa ttg   691
His Tyr Arg Glu Glu Leu Val Ala Leu Asp Glu Glu Val Thr Glu Leu
            185                 190                 195

ctc agc ggc gtg gcc cca gaa aac cgc aag ctg gta acc aat cac aat   739
Leu Ser Gly Val Ala Pro Glu Asn Arg Lys Leu Val Thr Asn His Asn
        200                 205                 210

gtt ttt gga tac ctg gcc agc cgg ttt aac tac acc gtc att gac acc   787
Val Phe Gly Tyr Leu Ala Ser Arg Phe Asn Tyr Thr Val Ile Asp Thr
    215                 220                 225

atc atc cca ggt gga agc aca ttg gcg gcg cct tca gca tct gac ctc   835
Ile Ile Pro Gly Gly Ser Thr Leu Ala Ala Pro Ser Ala Ser Asp Leu
230                 235                 240                 245

aat gac atc tcc acc gcc atc gaa gac aac aat gtt ccc gca atc ttc   883
Asn Asp Ile Ser Thr Ala Ile Glu Asp Asn Asn Val Pro Ala Ile Phe
                250                 255                 260

acc gat acc tca agc cca caa cgg tta gct gaa gtg ttg gcc agc aac   931
Thr Asp Thr Ser Ser Pro Gln Arg Leu Ala Glu Val Leu Ala Ser Asn
            265                 270                 275

gct ggc att gat gtt caa gtg gtg tcc att ttc acg gaa tca ctc acc   979
Ala Gly Ile Asp Val Gln Val Val Ser Ile Phe Thr Glu Ser Leu Thr
        280                 285                 290

gat gca gat ggt gaa gca ccc acc tac atc agc atg caa aaa atc aat   1027
Asp Ala Asp Gly Glu Ala Pro Thr Tyr Ile Ser Met Gln Lys Ile Asn
    295                 300                 305

gcc gag cgc att gca agc act ttg tcc taaacagtcc taaacagtct         1074
Ala Glu Arg Ile Ala Ser Thr Leu Ser
310                 315

taa                                                               1077
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<210> 2728
<211> 318
<212> PRT
<213> Corynebacterium glutamicum

<400> 2728

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Val Ile Leu Lys Asp Ile Phe Asn Asn Gly Glu Leu Phe Gly Ala Ser
  1               5                  10                  15

Ser Ala Lys Asn Phe Arg Lys Leu Leu Ala Val Pro Ala Val Ala Ala
             20                  25                  30

Ser Leu Ala Phe Gly Ile Thr Ala Cys Ser Ala Val Asp Asp Thr Pro
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         35                  40                  45

Asp Ile Val Val Thr Thr Asn Ile Leu Gly Asp Val Val Ser His Ile
     50                  55                  60

Val Gly Asp Ser Ala Asp Val Gln Val Leu Met Lys Pro Asn Ala Asp
 65                  70                  75                  80

Pro His Ser Phe Gly Val Ser Ala Gln Asp Ala Ala Ala Met Glu His
                85                  90                  95

Ala Asp Leu Ile Val Ala Asn Gly Leu Gly Leu Glu Glu Gly Leu Gln
            100                 105                 110

Ser Asn Val Asp Asn Ala Lys Ser Gln Gly Val Pro Val Leu Glu Val
        115                 120                 125

Gly Glu His Ile Asp Val Ile Asp Tyr Ser Pro Gly Val Pro Asp Pro
    130                 135                 140

His Phe Trp Thr Asp Pro Ala Arg Met Ile Ala Ala Thr Glu Val Ile
145                 150                 155                 160

Glu Ala Glu Leu Ile Lys Glu Leu Asp Pro Ser Leu Thr Glu Ser Ile
                165                 170                 175

Thr Gln Ser Ala Gln His Tyr Arg Glu Glu Leu Val Ala Leu Asp Glu
            180                 185                 190

Glu Val Thr Glu Leu Leu Ser Gly Val Ala Pro Glu Asn Arg Lys Leu
        195                 200                 205

Val Thr Asn His Asn Val Phe Gly Tyr Leu Ala Ser Arg Phe Asn Tyr
    210                 215                 220

Thr Val Ile Asp Thr Ile Ile Pro Gly Gly Ser Thr Leu Ala Ala Pro
225                 230                 235                 240

Ser Ala Ser Asp Leu Asn Asp Ile Ser Thr Ala Ile Glu Asp Asn Asn
                245                 250                 255

Val Pro Ala Ile Phe Thr Asp Thr Ser Ser Pro Gln Arg Leu Ala Glu
            260                 265                 270

Val Leu Ala Ser Asn Ala Gly Ile Asp Val Gln Val Val Ser Ile Phe
        275                 280                 285

Thr Glu Ser Leu Thr Asp Ala Asp Gly Glu Ala Pro Thr Tyr Ile Ser
    290                 295                 300

Met Gln Lys Ile Asn Ala Glu Arg Ile Ala Ser Thr Leu Ser
305                 310                 315
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<210> 2729
<211> 1401
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

<222> (101)..(1378)
<223> RXA02444

<400> 2729
aaaatcaatg ccgagcgcat tgcaagcact ttgtcctaaa cagtcctaaa cagtcttaaa 60

cagtccccgt tttactaaat gttttactaa aaggagaacc atg aaa aac tcc aag 115
Met Lys Asn Ser Lys
1 5

cta ctt ctt att gct gcg gta tcc acc gca tct atc ctg ctg gca agc 163
Leu Leu Leu Ile Ala Ala Val Ser Thr Ala Ser Ile Leu Leu Ala Ser
10 15 20

tgt ggc act gac agc tct gca gat act gca act gcg tct agc tct gca 211
Cys Gly Thr Asp Ser Ser Ala Asp Thr Ala Thr Ala Ser Ser Ser Ala
25 30 35

aca gca agc tcc gag gca cac gat cat gat ggc cac gaa gcc gaa ggc 259
Thr Ala Ser Ser Glu Ala His Asp His Asp Gly His Glu Ala Glu Gly
40 45 50

agc agc act gcc gtt gag gtg tcc tcc ccg cag gcc cgc atc gtc acc 307
Ser Ser Thr Ala Val Glu Val Ser Ser Pro Gln Ala Arg Ile Val Thr
55 60 65

acc tac gac ggt ggc atc att acc ctc gac gcc aac act ctg gaa atc 355
Thr Tyr Asp Gly Gly Ile Ile Thr Leu Asp Ala Asn Thr Leu Glu Ile
70 75 80 85

ctg gaa gac acc gaa cta gca ggt ttt aac cgc ctc aac agt gca gga 403
Leu Glu Asp Thr Glu Leu Ala Gly Phe Asn Arg Leu Asn Ser Ala Gly
90 95 100

gac gga cgc cac gta ttt gtc tcc aca ggt ggc ggc ttc cag ctc ttt 451
Asp Gly Arg His Val Phe Val Ser Thr Gly Gly Gly Phe Gln Leu Phe
105 110 115

gat acc ggc gca tgg acc gaa cca cac ggc gat cac acc cac agc tac 499
Asp Thr Gly Ala Trp Thr Glu Pro His Gly Asp His Thr His Ser Tyr
120 125 130

acc gcc acc cca gaa ctc acc gac atc acc tac tcc acc gat aag cct 547
Thr Ala Thr Pro Glu Leu Thr Asp Ile Thr Tyr Ser Thr Asp Lys Pro
135 140 145

ggt cat gta gtg aac cac gcc ggc aag acc gtg ctg ttc ggc gat ggt 595
Gly His Val Val Asn His Ala Gly Lys Thr Val Leu Phe Gly Asp Gly
150 155 160 165

gac ggc aaa atc cag atc ttc gac acc gct tcc ctc ctc aag ggc gat 643
Asp Gly Lys Ile Gln Ile Phe Asp Thr Ala Ser Leu Leu Lys Gly Asp
170 175 180

gaa gta gaa cct gag atc aaa aac gcc ctc aaa gcc cac cac ggc gtg 691
Glu Val Glu Pro Glu Ile Lys Asn Ala Leu Lys Ala His His Gly Val
185 190 195

gca gta gtc ctc gaa aac ggc gac ctg ctg cac act ttg ggc gat gag 739
Ala Val Val Leu Glu Asn Gly Asp Leu Leu His Thr Leu Gly Asp Glu
200 205 210

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gat tcc cgc aac ggc gcc gtc gta ttc aac gca gcc ggt gaa gaa atc   787
Asp Ser Arg Asn Gly Ala Val Val Phe Asn Ala Ala Gly Glu Glu Ile
    215                 220                 225

gcc cgc aac gaa cag tgc ccc ggc gtt cac ggt gaa agc gca gca ctc   835
Ala Arg Asn Glu Gln Cys Pro Gly Val His Gly Glu Ser Ala Ala Leu
230                 235                 240                 245

ggt gac gcc atc gca gtt ggc tgt gaa gac ggt gta ctg atc tac aag   883
Gly Asp Ala Ile Ala Val Gly Cys Glu Asp Gly Val Leu Ile Tyr Lys
                250                 255                 260

gac ggc gag ttc acc aag gtc cag gca cct gat tcc tac ggt cgc atc   931
Asp Gly Glu Phe Thr Lys Val Gln Ala Pro Asp Ser Tyr Gly Arg Ile
            265                 270                 275

ggc aac caa tca ggc agc gac gtc tct cct gtc gtc ctc ggc gat tac   979
Gly Asn Gln Ser Gly Ser Asp Val Ser Pro Val Val Leu Gly Asp Tyr
        280                 285                 290

aag gta gat aaa gac gcc gac ttg gag cgc cca gag cgc gtt tcc ctc   1027
Lys Val Asp Lys Asp Ala Asp Leu Glu Arg Pro Glu Arg Val Ser Leu
    295                 300                 305

acc aac acc gag acc ggc gag ctc acc ctc gtt gac ctc ggc acc tcc   1075
Thr Asn Thr Glu Thr Gly Glu Leu Thr Leu Val Asp Leu Gly Thr Ser
310                 315                 320                 325

tac tcc ttc cgc tca ctt ggc cgt ggc cct gca ggc gaa gca gta gtt   1123
Tyr Ser Phe Arg Ser Leu Gly Arg Gly Pro Ala Gly Glu Ala Val Val
                330                 335                 340

cta ggc acc gac ggc gca ctc cac atc atc gat gcc aac acc ggc gcc   1171
Leu Gly Thr Asp Gly Ala Leu His Ile Ile Asp Ala Asn Thr Gly Ala
            345                 350                 355

atc acc aac acc tac ccc gtc atc gat gcc tgg acc gaa cca gaa gta   1219
Ile Thr Asn Thr Tyr Pro Val Ile Asp Ala Trp Thr Glu Pro Glu Val
        360                 365                 370

tgg caa gaa gca cgc cca acc ctg ttc atc aac aag gac cgc gca tac   1267
Trp Gln Glu Ala Arg Pro Thr Leu Phe Ile Asn Lys Asp Arg Ala Tyr
    375                 380                 385

gtc tcc gac cca tca aac aac gaa ctc cat gtt gtt gac ctg gcc aac   1315
Val Ser Asp Pro Ser Asn Asn Glu Leu His Val Val Asp Leu Ala Asn
390                 395                 400                 405

ggc aac atc ctt gcc agc gcc acc ctg cca gga acc ccc aac gag ctc   1363
Gly Asn Ile Leu Ala Ser Ala Thr Leu Pro Gly Thr Pro Asn Glu Leu
                410                 415                 420

acc gga gtg agc ggc taaaaagaaa ttgcttttcg acg                    1401
Thr Gly Val Ser Gly
            425
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<210> 2730
<211> 426
<212> PRT

<213> Corynebacterium glutamicum

<400> 2730

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Met Lys Asn Ser Lys Leu Leu Leu Ile Ala Ala Val Ser Thr Ala Ser
  1               5                  10                  15

Ile Leu Leu Ala Ser Cys Gly Thr Asp Ser Ser Ala Asp Thr Ala Thr
             20                  25                  30

Ala Ser Ser Ser Ala Thr Ala Ser Ser Glu Ala His Asp His Asp Gly
         35                  40                  45

His Glu Ala Glu Gly Ser Ser Thr Ala Val Glu Val Ser Ser Pro Gln
     50                  55                  60

Ala Arg Ile Val Thr Thr Tyr Asp Gly Gly Ile Ile Thr Leu Asp Ala
 65                  70                  75                  80

Asn Thr Leu Glu Ile Leu Glu Asp Thr Glu Leu Ala Gly Phe Asn Arg
                 85                  90                  95

Leu Asn Ser Ala Gly Asp Gly Arg His Val Phe Val Ser Thr Gly Gly
            100                 105                 110

Gly Phe Gln Leu Phe Asp Thr Gly Ala Trp Thr Glu Pro His Gly Asp
        115                 120                 125

His Thr His Ser Tyr Thr Ala Thr Pro Glu Leu Thr Asp Ile Thr Tyr
    130                 135                 140

Ser Thr Asp Lys Pro Gly His Val Val Asn His Ala Gly Lys Thr Val
145                 150                 155                 160

Leu Phe Gly Asp Gly Asp Gly Lys Ile Gln Ile Phe Asp Thr Ala Ser
                165                 170                 175

Leu Leu Lys Gly Asp Glu Val Glu Pro Glu Ile Lys Asn Ala Leu Lys
            180                 185                 190

Ala His His Gly Val Ala Val Val Leu Glu Asn Gly Asp Leu Leu His
        195                 200                 205

Thr Leu Gly Asp Glu Asp Ser Arg Asn Gly Ala Val Val Phe Asn Ala
    210                 215                 220

Ala Gly Glu Glu Ile Ala Arg Asn Glu Gln Cys Pro Gly Val His Gly
225                 230                 235                 240

Glu Ser Ala Ala Leu Gly Asp Ala Ile Ala Val Gly Cys Glu Asp Gly
                245                 250                 255

Val Leu Ile Tyr Lys Asp Gly Glu Phe Thr Lys Val Gln Ala Pro Asp
            260                 265                 270

Ser Tyr Gly Arg Ile Gly Asn Gln Ser Gly Ser Asp Val Ser Pro Val
        275                 280                 285

Val Leu Gly Asp Tyr Lys Val Asp Lys Asp Ala Asp Leu Glu Arg Pro
    290                 295                 300

Glu Arg Val Ser Leu Thr Asn Thr Glu Thr Gly Glu Leu Thr Leu Val
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305                 310                 315                 320

Asp Leu Gly Thr Ser Tyr Ser Phe Arg Ser Leu Gly Arg Gly Pro Ala
                325                 330                 335

Gly Glu Ala Val Val Leu Gly Thr Asp Gly Ala Leu His Ile Ile Asp
            340                 345                 350

Ala Asn Thr Gly Ala Ile Thr Asn Thr Tyr Pro Val Ile Asp Ala Trp
        355                 360                 365

Thr Glu Pro Glu Val Trp Gln Glu Ala Arg Pro Thr Leu Phe Ile Asn
    370                 375                 380

Lys Asp Arg Ala Tyr Val Ser Asp Pro Ser Asn Asn Glu Leu His Val
385                 390                 395                 400

Val Asp Leu Ala Asn Gly Asn Ile Leu Ala Ser Ala Thr Leu Pro Gly
                405                 410                 415

Thr Pro Asn Glu Leu Thr Gly Val Ser Gly
            420                 425
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Sequence Listing

<210> 2731
<211> 303
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(280)
<223> RXA02452

<400> 2731

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tagggtggaa tgcagaaata tttcctacgg aaggtccgtt atg acg cct gca ggt   115
                                              Met Thr Pro Ala Gly
                                                1               5

cca gca caa tta ctc att gtt gct ctt gta gta att gtc ctc ttt ggt   163
Pro Ala Gln Leu Leu Ile Val Ala Leu Val Val Ile Val Leu Phe Gly
                10                  15                  20

tcc aat aag ttg cct gat gtt gct cgg tcc gtt ggc cgt tcg atg cgc   211
Ser Asn Lys Leu Pro Asp Val Ala Arg Ser Val Gly Arg Ser Met Arg
            25                  30                  35

att ttc aaa tct gag atc aaa gag atg aac aag gat cag atc gaa agc   259
Ile Phe Lys Ser Glu Ile Lys Glu Met Asn Lys Asp Gln Ile Glu Ser
        40                  45                  50

tcc gat cag acc ttg aag aac taaggttcct cgcatctaaa aac             303
Ser Asp Gln Thr Leu Lys Asn
    55                  60
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<210> 2732
<211> 60
<212> PRT

<213> Corynebacterium glutamicum

<400> 2732

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Met Thr Pro Ala Gly Pro Ala Gln Leu Leu Ile Val Ala Leu Val Val
  1               5                  10                  15

Ile Val Leu Phe Gly Ser Asn Lys Leu Pro Asp Val Ala Arg Ser Val
             20                  25                  30

Gly Arg Ser Met Arg Ile Phe Lys Ser Glu Ile Lys Glu Met Asn Lys
         35                  40                  45

Asp Gln Ile Glu Ser Ser Asp Gln Thr Leu Lys Asn
     50                  55                  60
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<210> 2733
<211> 858
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(835)
<223> RXA02459

<400> 2733

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ggtgcgatca ttggcctcgc ggttgatggc gttcaggttg aagacattaa gaccacttcc 60

aaaactttcc ctggttttga aaatgtttgg gaggagatgg ttg gct aga cgc agc   115
                                              Leu Ala Arg Arg Ser
                                                1               5

tat gac gaa tcc gat gtt cgt gtt cgc cca ggt aaa ggt acc cgc cct   163
Tyr Asp Glu Ser Asp Val Arg Val Arg Pro Gly Lys Gly Thr Arg Pro
                10                  15                  20

cgt acg aag gat cgg cca tcg cat gag aat gct cta gtg ggc atg gtt   211
Arg Thr Lys Asp Arg Pro Ser His Glu Asn Ala Leu Val Gly Met Val
            25                  30                  35

gtg acg aag gat cgt ggt cgt tgg ggt gtt gtt ctc gat ggt cgt caa   259
Val Thr Lys Asp Arg Gly Arg Trp Gly Val Val Leu Asp Gly Arg Gln
        40                  45                  50

gat gcc att gtg acg atg cgt gcc cgt gag ttg ggg cgt acg gct atc   307
Asp Ala Ile Val Thr Met Arg Ala Arg Glu Leu Gly Arg Thr Ala Ile
    55                  60                  65

gaa gtg ggt gat cgt gtc gga gtt gtc ggc gat acg tct ggc cgt ccg   355
Glu Val Gly Asp Arg Val Gly Val Val Gly Asp Thr Ser Gly Arg Pro
70                  75                  80                  85

ggc tcg ttg gct cga att gtc cgc ctt gag gag cgc acg agt gtg ttg   403
Gly Ser Leu Ala Arg Ile Val Arg Leu Glu Glu Arg Thr Ser Val Leu
                90                  95                  100

cgt cgt acg gct gat gac acg gac ccg ttt gag cgg att gtg gtg gct   451
Arg Arg Thr Ala Asp Asp Thr Asp Pro Phe Glu Arg Ile Val Val Ala
            105                 110                 115
```

```
aat gcg gat cag ttg ttg att gtt tct gct gtc gcc gat ccg ccg cct   499
Asn Ala Asp Gln Leu Leu Ile Val Ser Ala Val Ala Asp Pro Pro Pro
        120                 125                 130

cgg gcg ggt ttt gtg gag cgt gct cta att gct gcg ttt gtt ggt aat   547
Arg Ala Gly Phe Val Glu Arg Ala Leu Ile Ala Ala Phe Val Gly Asn
    135                 140                 145

ttg cag ccg gtg ttg tgt ttg acg aag tct gat ttg gcg gat cct gcg   595
Leu Gln Pro Val Leu Cys Leu Thr Lys Ser Asp Leu Ala Asp Pro Ala
150                 155                 160                 165

gag ttc gct gcg gag ttt gag gct ttg gaa gtg ccg gtt gtt gtt tgt   643
Glu Phe Ala Ala Glu Phe Glu Ala Leu Glu Val Pro Val Val Val Cys
                170                 175                 180

ggt gtt gat gat cct ctt gat cct gtt ttg gag gtc gtg gaa ggc cat   691
Gly Val Asp Asp Pro Leu Asp Pro Val Leu Glu Val Val Glu Gly His
            185                 190                 195

att acg gcg ctt att ggg caa tct ggt gtg ggt aag tcg acg ttg gtt   739
Ile Thr Ala Leu Ile Gly Gln Ser Gly Val Gly Lys Ser Thr Leu Val
        200                 205                 210

aat cgt ttg gtg ccg gaa tgc cga tcg tta aac tgg tgt cgt gtc ggg   787
Asn Arg Leu Val Pro Glu Cys Arg Ser Leu Asn Trp Cys Arg Val Gly
    215                 220                 225

ggt tgg caa ggg tcg gca tac gtc gac gca gtc ggt cgc tct tgc cat   835
Gly Trp Gln Gly Ser Ala Tyr Val Asp Ala Val Gly Arg Ser Cys His
230                 235                 240                 245

tgataatggt tggattatcg aaa                                       858


<210> 2734
<211> 245
<212> PRT
<213> Corynebacterium glutamicum

<400> 2734
Leu Ala Arg Arg Ser Tyr Asp Glu Ser Asp Val Arg Val Arg Pro Gly
  1               5                  10                  15

Lys Gly Thr Arg Pro Arg Thr Lys Asp Arg Pro Ser His Glu Asn Ala
             20                  25                  30

Leu Val Gly Met Val Val Thr Lys Asp Arg Gly Arg Trp Gly Val Val
         35                  40                  45

Leu Asp Gly Arg Gln Asp Ala Ile Val Thr Met Arg Ala Arg Glu Leu
     50                  55                  60

Gly Arg Thr Ala Ile Glu Val Gly Asp Arg Val Gly Val Val Gly Asp
 65                  70                  75                  80

Thr Ser Gly Arg Pro Gly Ser Leu Ala Arg Ile Val Arg Leu Glu Glu
                 85                  90                  95

Arg Thr Ser Val Leu Arg Arg Thr Ala Asp Asp Thr Asp Pro Phe Glu
            100                 105                 110
```

```
Arg Ile Val Val Ala Asn Ala Asp Gln Leu Leu Ile Val Ser Ala Val
        115                 120                 125

Ala Asp Pro Pro Pro Arg Ala Gly Phe Val Glu Arg Ala Leu Ile Ala
    130                 135                 140

Ala Phe Val Gly Asn Leu Gln Pro Val Leu Cys Leu Thr Lys Ser Asp
145                 150                 155                 160

Leu Ala Asp Pro Ala Glu Phe Ala Ala Glu Phe Glu Ala Leu Glu Val
                165                 170                 175

Pro Val Val Val Cys Gly Val Asp Asp Pro Leu Asp Pro Val Leu Glu
            180                 185                 190

Val Val Glu Gly His Ile Thr Ala Leu Ile Gly Gln Ser Gly Val Gly
        195                 200                 205

Lys Ser Thr Leu Val Asn Arg Leu Val Pro Glu Cys Arg Ser Leu Asn
    210                 215                 220

Trp Cys Arg Val Gly Gly Trp Gln Gly Ser Ala Tyr Val Asp Ala Val
225                 230                 235                 240

Gly Arg Ser Cys His
                245
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<210> 2735
<211> 531
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(508)
<223> RXA02461

<400> 2735

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agaaaatctc aaggcaaaaa acaagccacc ccaatctgtg cgacaatcaa accacagact 60

acgactatta tgtcacgaag aaaccaaaga aagggaaata atg cgc gga cta att   115
                                               Met Arg Gly Leu Ile
                                                 1               5

gtt gac tac gct gga gta cta gac gga acc gat gag gac cag cgt cgc   163
Val Asp Tyr Ala Gly Val Leu Asp Gly Thr Asp Glu Asp Gln Arg Arg
                 10                  15                  20

tgg cgc aac ctg ctc gcc gca gca aag aaa aat ggc gtc gga acc gtg   211
Trp Arg Asn Leu Leu Ala Ala Ala Lys Lys Asn Gly Val Gly Thr Val
             25                  30                  35

atc ctc agc aac gat cca ggt ggg ctc ggc gca gcg ccg atc cgg gaa   259
Ile Leu Ser Asn Asp Pro Gly Gly Leu Gly Ala Ala Pro Ile Arg Glu
         40                  45                  50

ctc gaa aca aac ggg gta gtc gat aag gtg ctg ctg tcg gga gaa ctt   307
Leu Glu Thr Asn Gly Val Val Asp Lys Val Leu Leu Ser Gly Glu Leu
     55                  60                  65
```

```
ggc gtc gaa aag cca gag gaa gca gct ttc cag gcc gcc gca gac gcc   355
Gly Val Glu Lys Pro Glu Glu Ala Ala Phe Gln Ala Ala Ala Asp Ala
 70                  75                  80                  85

atc gac ctg ccc atg cgt gac tgc gtg ctt gtc gac gac tcg atc ctc   403
Ile Asp Leu Pro Met Arg Asp Cys Val Leu Val Asp Asp Ser Ile Leu
                90                  95                 100

aac gtg cgc ggc gcc gtc gaa gcc gga ctc gta ggc gtc tac tac cag   451
Asn Val Arg Gly Ala Val Glu Ala Gly Leu Val Gly Val Tyr Tyr Gln
            105                 110                 115

caa ttt gac cgt gca gtc gtc gaa atc gtc gga ctg ttc ggg cta gaa   499
Gln Phe Asp Arg Ala Val Val Glu Ile Val Gly Leu Phe Gly Leu Glu
        120                 125                 130

gga gaa ttc taatcttgcg cgtctacatc cca                            531
Gly Glu Phe
    135
```

<210> 2736
<211> 136
<212> PRT
<213> Corynebacterium glutamicum

<400> 2736

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Met Arg Gly Leu Ile Val Asp Tyr Ala Gly Val Leu Asp Gly Thr Asp
  1               5                  10                  15

Glu Asp Gln Arg Arg Trp Arg Asn Leu Leu Ala Ala Ala Lys Lys Asn
             20                  25                  30

Gly Val Gly Thr Val Ile Leu Ser Asn Asp Pro Gly Gly Leu Gly Ala
         35                  40                  45

Ala Pro Ile Arg Glu Leu Glu Thr Asn Gly Val Val Asp Lys Val Leu
     50                  55                  60

Leu Ser Gly Glu Leu Gly Val Glu Lys Pro Glu Glu Ala Ala Phe Gln
 65                  70                  75                  80

Ala Ala Ala Asp Ala Ile Asp Leu Pro Met Arg Asp Cys Val Leu Val
                 85                  90                  95

Asp Asp Ser Ile Leu Asn Val Arg Gly Ala Val Glu Ala Gly Leu Val
            100                 105                 110

Gly Val Tyr Tyr Gln Gln Phe Asp Arg Ala Val Val Glu Ile Val Gly
        115                 120                 125

Leu Phe Gly Leu Glu Gly Glu Phe
    130                 135
```

<210> 2737
<211> 348
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(325)
<223> RXA02467

<400> 2737
gtgaacgtag gtctggggct ttcagaagac acaacttaga tactatcgtt gcacggttac 60

aatagggtca ttccaataca acgattcttt taggagagct atg gat atc aag atc 115
Met Asp Ile Lys Ile
1 5

gga ttt gcc gat act gcc cgt gaa ctg gtc att tct tct gct ttg cag 163
Gly Phe Ala Asp Thr Ala Arg Glu Leu Val Ile Ser Ser Ala Leu Gln
10 15 20

cag gat gag gcc gct gcg aag gtg tcg gag gct ttg gct aat gat tct 211
Gln Asp Glu Ala Ala Ala Lys Val Ser Glu Ala Leu Ala Asn Asp Ser
25 30 35

ggc gtt tta gat ttg agc gat gaa aag ggt cgc cgt tac att att cgt 259
Gly Val Leu Asp Leu Ser Asp Glu Lys Gly Arg Arg Tyr Ile Ile Arg
40 45 50

aat agc cga atc gct tat gtt gag gtc ggc acg agt gct cct cgt act 307
Asn Ser Arg Ile Ala Tyr Val Glu Val Gly Thr Ser Ala Pro Arg Thr
55 60 65

gtc ggc ttc gct ggc gca taggggcttt tagacacgtg tcg 348
Val Gly Phe Ala Gly Ala
70 75

<210> 2738
<211> 75
<212> PRT
<213> Corynebacterium glutamicum

<400> 2738
Met Asp Ile Lys Ile Gly Phe Ala Asp Thr Ala Arg Glu Leu Val Ile
1 5 10 15

Ser Ser Ala Leu Gln Gln Asp Glu Ala Ala Ala Lys Val Ser Glu Ala
20 25 30

Leu Ala Asn Asp Ser Gly Val Leu Asp Leu Ser Asp Glu Lys Gly Arg
35 40 45

Arg Tyr Ile Ile Arg Asn Ser Arg Ile Ala Tyr Val Glu Val Gly Thr
50 55 60

Ser Ala Pro Arg Thr Val Gly Phe Ala Gly Ala
65 70 75

<210> 2739
<211> 414
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS
<222> (101)..(391)
<223> RXA02472

<400> 2739
atgattctca taaggctata aacaatgtag ttaggttaca ctaatggtgt ccggttgtga 60

atagtgcagc ggacggggtt ccgctgcgga ggaggtcatc atg tca ttt gtt aac 115
Met Ser Phe Val Asn
1 5

atc acg gct ctt acg ttc cct gca ggg gct gaa aaa gaa atc gaa caa 163
Ile Thr Ala Leu Thr Phe Pro Ala Gly Ala Glu Lys Glu Ile Glu Gln
10 15 20

cgc ttc gcg gct cgt aag aag gct gta gat acg gcc aaa gga ttc caa 211
Arg Phe Ala Ala Arg Lys Lys Ala Val Asp Thr Ala Lys Gly Phe Gln
25 30 35

gaa ttt gag ttg ttg cgt cca caa ttt ggt gag gat cgc tac ttc gta 259
Glu Phe Glu Leu Leu Arg Pro Gln Phe Gly Glu Asp Arg Tyr Phe Val
40 45 50

gtt act cgt tgg gat tcc cgc gaa gac tat caa gca tgg tcg gat gcc 307
Val Thr Arg Trp Asp Ser Arg Glu Asp Tyr Gln Ala Trp Ser Asp Ala
55 60 65

cgc cct gcc ggt aac cat gct gat gat gaa caa cgt ggc atg agc gtg 355
Arg Pro Ala Gly Asn His Ala Asp Asp Glu Gln Arg Gly Met Ser Val
70 75 80 85

gaa gtt ctt ggt ttc gat gtg gtt cct ttg gaa ggc taaaagtcct 401
Glu Val Leu Gly Phe Asp Val Val Pro Leu Glu Gly
90 95

tggcgtggca tag 414

<210> 2740
<211> 97
<212> PRT
<213> Corynebacterium glutamicum

<400> 2740
Met Ser Phe Val Asn Ile Thr Ala Leu Thr Phe Pro Ala Gly Ala Glu
1 5 10 15

Lys Glu Ile Glu Gln Arg Phe Ala Ala Arg Lys Lys Ala Val Asp Thr
20 25 30

Ala Lys Gly Phe Gln Glu Phe Glu Leu Leu Arg Pro Gln Phe Gly Glu
35 40 45

Asp Arg Tyr Phe Val Val Thr Arg Trp Asp Ser Arg Glu Asp Tyr Gln
50 55 60

Ala Trp Ser Asp Ala Arg Pro Ala Gly Asn His Ala Asp Asp Glu Gln
65 70 75 80

Arg Gly Met Ser Val Glu Val Leu Gly Phe Asp Val Val Pro Leu Glu
85 90 95

Gly

<210> 2741
<211> 864
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(841)
<223> RXA02473

<400> 2741
tgcagttatg attaaactaa ctcctagcag tggccaacta catgtctggc ttaatagcct 60

atgaacgcct aagcctggag ccacaacaac cacattccga atg gtc gca gag tac 115
Met Val Ala Glu Tyr
1 5

cct gac gga tcc tcg gaa ata ttc ccg gta acg tta aat tta att ccg 163
Pro Asp Gly Ser Ser Glu Ile Phe Pro Val Thr Leu Asn Leu Ile Pro
10 15 20

gaa gat acc ctc gtt tat gac gcc gtc tac aaa ttc aaa agc atc cga 211
Glu Asp Thr Leu Val Tyr Asp Ala Val Tyr Lys Phe Lys Ser Ile Arg
25 30 35

act ggt tcc gaa gat caa ata acc cca ttt gta tca aac caa cct gat 259
Thr Gly Ser Glu Asp Gln Ile Thr Pro Phe Val Ser Asn Gln Pro Asp
40 45 50

gtg cct ttc cct gca gga aca tcg ttc aca tta act gga tat tat gaa 307
Val Pro Phe Pro Ala Gly Thr Ser Phe Thr Leu Thr Gly Tyr Tyr Glu
55 60 65

att gat cag ctg aga agt gca gga tgg aaa ttt gag ctt aat cct gta 355
Ile Asp Gln Leu Arg Ser Ala Gly Trp Lys Phe Glu Leu Asn Pro Val
70 75 80 85

aca ggt gaa ctt tca gtc aca gtt cct atc tct gta att tac cct gat 403
Thr Gly Glu Leu Ser Val Thr Val Pro Ile Ser Val Ile Tyr Pro Asp
90 95 100

ggg tct cgt gat aac aca atc gcg acc atg gaa tcc gta ggc cct gat 451
Gly Ser Arg Asp Asn Thr Ile Ala Thr Met Glu Ser Val Gly Pro Asp
105 110 115

gat tct gag ctt ttc aaa cca gac ttt gat tta atc cca ata aaa tca 499
Asp Ser Glu Leu Phe Lys Pro Asp Phe Asp Leu Ile Pro Ile Lys Ser
120 125 130

ggt gac tat ata gag ata ggt gta ctc gca cca ggg ctt cct gct ggt 547
Gly Asp Tyr Ile Glu Ile Gly Val Leu Ala Pro Gly Leu Pro Ala Gly
135 140 145

acg gaa ttc cat ctc gat tac tac gca ctt ccg gat cga ttc ttt gac 595
Thr Glu Phe His Leu Asp Tyr Tyr Ala Leu Pro Asp Arg Phe Phe Asp
150 155 160 165

```
tta ggc ggt tct aca agc ctt tca ggc aac ggt aag ttc tct ctt gga   643
Leu Gly Gly Ser Thr Ser Leu Ser Gly Asn Gly Lys Phe Ser Leu Gly
                170                 175                 180

gtt cca ctt acc tgg aat gat gat ctc cag ctc ccg atc tcg att act   691
Val Pro Leu Thr Trp Asn Asp Asp Leu Gln Leu Pro Ile Ser Ile Thr
            185                 190                 195

ttt cct gac gga agc cac aca gtt gag aat ttg cat gtt gac gta acc   739
Phe Pro Asp Gly Ser His Thr Val Glu Asn Leu His Val Asp Val Thr
        200                 205                 210

ccc gca aac ttt gct ggc aac ccc att gac gag cct aag gac gat gac   787
Pro Ala Asn Phe Ala Gly Asn Pro Ile Asp Glu Pro Lys Asp Asp Asp
    215                 220                 225

aag gat cat cca caa ccg gct cct aaa cca agt ggc agc tca ttt ggt   835
Lys Asp His Pro Gln Pro Ala Pro Lys Pro Ser Gly Ser Ser Phe Gly
230                 235                 240                 245

tct agc tagttcctac taaacagttc aaa                                864
Ser Ser
```

<210> 2742
<211> 247
<212> PRT
<213> Corynebacterium glutamicum

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<400> 2742
Met Val Ala Glu Tyr Pro Asp Gly Ser Ser Glu Ile Phe Pro Val Thr
  1               5                  10                  15

Leu Asn Leu Ile Pro Glu Asp Thr Leu Val Tyr Asp Ala Val Tyr Lys
             20                  25                  30

Phe Lys Ser Ile Arg Thr Gly Ser Glu Asp Gln Ile Thr Pro Phe Val
         35                  40                  45

Ser Asn Gln Pro Asp Val Pro Phe Pro Ala Gly Thr Ser Phe Thr Leu
     50                  55                  60

Thr Gly Tyr Tyr Glu Ile Asp Gln Leu Arg Ser Ala Gly Trp Lys Phe
 65                  70                  75                  80

Glu Leu Asn Pro Val Thr Gly Glu Leu Ser Val Thr Val Pro Ile Ser
                 85                  90                  95

Val Ile Tyr Pro Asp Gly Ser Arg Asp Asn Thr Ile Ala Thr Met Glu
            100                 105                 110

Ser Val Gly Pro Asp Asp Ser Glu Leu Phe Lys Pro Asp Phe Asp Leu
        115                 120                 125

Ile Pro Ile Lys Ser Gly Asp Tyr Ile Glu Ile Gly Val Leu Ala Pro
    130                 135                 140

Gly Leu Pro Ala Gly Thr Glu Phe His Leu Asp Tyr Tyr Ala Leu Pro
145                 150                 155                 160
```

```
Asp Arg Phe Phe Asp Leu Gly Gly Ser Thr Ser Leu Ser Gly Asn Gly
                165                 170                 175

Lys Phe Ser Leu Gly Val Pro Leu Thr Trp Asn Asp Asp Leu Gln Leu
            180                 185                 190

Pro Ile Ser Ile Thr Phe Pro Asp Gly Ser His Thr Val Glu Asn Leu
        195                 200                 205

His Val Asp Val Thr Pro Ala Asn Phe Ala Gly Asn Pro Ile Asp Glu
    210                 215                 220

Pro Lys Asp Asp Asp Lys Asp His Pro Gln Pro Ala Pro Lys Pro Ser
225                 230                 235                 240

Gly Ser Ser Phe Gly Ser Ser
                245
```

<210> 2743
<211> 1278
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1255)
<223> RXA02475

<400> 2743

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tcgctcattg aggacggact cgcggaacaa aatgaggcgg gttatttcca cctgccacgg 60

taaaccactg cgcgcctgca aaaaacagta ggtttaagta atg ctt ggt ctc tct   115
                                               Met Leu Gly Leu Ser
                                                 1               5

cgt cgt aag ttt gcc atg ctc gct gcc tta act gcg gga atc gtt ggc   163
Arg Arg Lys Phe Ala Met Leu Ala Ala Leu Thr Ala Gly Ile Val Gly
                 10                  15                  20

gtt gtt gcc act ggt tgt agt acg ccc gca gaa cct gaa acg atc gat   211
Val Val Ala Thr Gly Cys Ser Thr Pro Ala Glu Pro Glu Thr Ile Asp
             25                  30                  35

aat ccg gtg ttc att ggt atc tcc atc gat cca att aaa aac cta agt   259
Asn Pro Val Phe Ile Gly Ile Ser Ile Asp Pro Ile Lys Asn Leu Ser
         40                  45                  50

ccg aat cac gct gca aac ctc ttc gct tta tct gca gat ggc tcg gga   307
Pro Asn His Ala Ala Asn Leu Phe Ala Leu Ser Ala Asp Gly Ser Gly
     55                  60                  65

gga att ttc caa gaa ctc gct ccc aca tac ttt ccg tcg atc cat cga   355
Gly Ile Phe Gln Glu Leu Ala Pro Thr Tyr Phe Pro Ser Ile His Arg
 70                  75                  80                  85

tta gga aac gga ttc atc gca ccc gat aga gat tct ttg gta gtt gtc   403
Leu Gly Asn Gly Phe Ile Ala Pro Asp Arg Asp Ser Leu Val Val Val
                 90                  95                 100
```

```
gac gct tct cta aag gaa gtt tat cga cac gaa gtg gcc agg ctt ggt   451
Asp Ala Ser Leu Lys Glu Val Tyr Arg His Glu Val Ala Arg Leu Gly
            105                 110                 115

gtt gga atg caa act caa tca gct agg tct cca ctg cat aaa tca gtt   499
Val Gly Met Gln Thr Gln Ser Ala Arg Ser Pro Leu His Lys Ser Val
        120                 125                 130

gcc ttc tcc ttc aat gaa gga aca gct gaa gcc cca tat aga cac cgc   547
Ala Phe Ser Phe Asn Glu Gly Thr Ala Glu Ala Pro Tyr Arg His Arg
    135                 140                 145

atc gtc tcc gca act gag aaa aca tca gct tcc gca atg aca gat cag   595
Ile Val Ser Ala Thr Glu Lys Thr Ser Ala Ser Ala Met Thr Asp Gln
150                 155                 160                 165

cgg cac ttc gcg ctt act gca tgc gat gac gga tcc aca cgg tgg gtc   643
Arg His Phe Ala Leu Thr Ala Cys Asp Asp Gly Ser Thr Arg Trp Val
                170                 175                 180

gaa tat tcc cct gac cgc gga atg gaa gat cca atg ggc ccc ggc tca   691
Glu Tyr Ser Pro Asp Arg Gly Met Glu Asp Pro Met Gly Pro Gly Ser
            185                 190                 195

gca cgc atc gtg act ctc cag gcc gac gga gaa ctc agt gaa att gac   739
Ala Arg Ile Val Thr Leu Gln Ala Asp Gly Glu Leu Ser Glu Ile Asp
        200                 205                 210

gtt gag tgg aat ttc ccg gat cgg ccc tcc gcc cca att att ctg tct   787
Val Glu Trp Asn Phe Pro Asp Arg Pro Ser Ala Pro Ile Ile Leu Ser
    215                 220                 225

tgc gaa gat cca agc gct tat ata gtt tca gaa gaa gac atc atc tat   835
Cys Glu Asp Pro Ser Ala Tyr Ile Val Ser Glu Glu Asp Ile Ile Tyr
230                 235                 240                 245

gta aaa gac gag gta agc cct gcc gaa tcc ata gga aaa tta cct gca   883
Val Lys Asp Glu Val Ser Pro Ala Glu Ser Ile Gly Lys Leu Pro Ala
                250                 255                 260

tat gaa att ccg gac cgc gcc cga ttc gat aca gtt tcc ggc gaa gac   931
Tyr Glu Ile Pro Asp Arg Ala Arg Phe Asp Thr Val Ser Gly Glu Asp
            265                 270                 275

tac ttc gct ttt acg tca act ggg atg ctg aca cgc atc aat att ccc   979
Tyr Phe Ala Phe Thr Ser Thr Gly Met Leu Thr Arg Ile Asn Ile Pro
        280                 285                 290

caa gca aaa atc gtc tac gca caa tcc att gac ctc tac ggc aag cat   1027
Gln Ala Lys Ile Val Tyr Ala Gln Ser Ile Asp Leu Tyr Gly Lys His
    295                 300                 305

ccg gtt tcc ata act ttc gat tcc gac cgt gca tac gtg gtt act tcc   1075
Pro Val Ser Ile Thr Phe Asp Ser Asp Arg Ala Tyr Val Val Thr Ser
310                 315                 320                 325

ggg gat tcc ggg gaa agc ctt ctt gaa atc gac ttg aat gat cca aca   1123
Gly Asp Ser Gly Glu Ser Leu Leu Glu Ile Asp Leu Asn Asp Pro Thr
                330                 335                 340

tgc act tca gat cag ctc tcg ctc act ggt ttc aac aaa tta ctc aca   1171
```

```
Cys Thr Ser Asp Gln Leu Ser Leu Thr Gly Phe Asn Lys Leu Leu Thr
            345                 350                 355

gct cgg aaa cct aag cca gaa ccg tcg atc atc atc gaa acc atc ttg   1219
Ala Arg Lys Pro Lys Pro Glu Pro Ser Ile Ile Ile Glu Thr Ile Leu
        360                 365                 370

cca att gac cca aac tac tca ctg ggt tgt aag agt tagattttgg        1265
Pro Ile Asp Pro Asn Tyr Ser Leu Gly Cys Lys Ser
    375                 380                 385

acggaagtgt gta                                                   1278


<210> 2744
<211> 385
<212> PRT
<213> Corynebacterium glutamicum

<400> 2744
Met Leu Gly Leu Ser Arg Arg Lys Phe Ala Met Leu Ala Ala Leu Thr
  1               5                  10                  15

Ala Gly Ile Val Gly Val Val Ala Thr Gly Cys Ser Thr Pro Ala Glu
             20                  25                  30

Pro Glu Thr Ile Asp Asn Pro Val Phe Ile Gly Ile Ser Ile Asp Pro
         35                  40                  45

Ile Lys Asn Leu Ser Pro Asn His Ala Ala Asn Leu Phe Ala Leu Ser
     50                  55                  60

Ala Asp Gly Ser Gly Gly Ile Phe Gln Glu Leu Ala Pro Thr Tyr Phe
 65                  70                  75                  80

Pro Ser Ile His Arg Leu Gly Asn Gly Phe Ile Ala Pro Asp Arg Asp
                 85                  90                  95

Ser Leu Val Val Val Asp Ala Ser Leu Lys Glu Val Tyr Arg His Glu
            100                 105                 110

Val Ala Arg Leu Gly Val Gly Met Gln Thr Gln Ser Ala Arg Ser Pro
        115                 120                 125

Leu His Lys Ser Val Ala Phe Ser Phe Asn Glu Gly Thr Ala Glu Ala
    130                 135                 140

Pro Tyr Arg His Arg Ile Val Ser Ala Thr Glu Lys Thr Ser Ala Ser
145                 150                 155                 160

Ala Met Thr Asp Gln Arg His Phe Ala Leu Thr Ala Cys Asp Asp Gly
                165                 170                 175

Ser Thr Arg Trp Val Glu Tyr Ser Pro Asp Arg Gly Met Glu Asp Pro
            180                 185                 190

Met Gly Pro Gly Ser Ala Arg Ile Val Thr Leu Gln Ala Asp Gly Glu
        195                 200                 205

Leu Ser Glu Ile Asp Val Glu Trp Asn Phe Pro Asp Arg Pro Ser Ala
    210                 215                 220
```

```
Pro Ile Ile Leu Ser Cys Glu Asp Pro Ser Ala Tyr Ile Val Ser Glu
225                 230                 235                 240

Glu Asp Ile Ile Tyr Val Lys Asp Glu Val Ser Pro Ala Glu Ser Ile
                245                 250                 255

Gly Lys Leu Pro Ala Tyr Glu Ile Pro Asp Arg Ala Arg Phe Asp Thr
            260                 265                 270

Val Ser Gly Glu Asp Tyr Phe Ala Phe Thr Ser Thr Gly Met Leu Thr
        275                 280                 285

Arg Ile Asn Ile Pro Gln Ala Lys Ile Val Tyr Ala Gln Ser Ile Asp
    290                 295                 300

Leu Tyr Gly Lys His Pro Val Ser Ile Thr Phe Asp Ser Asp Arg Ala
305                 310                 315                 320

Tyr Val Val Thr Ser Gly Asp Ser Gly Glu Ser Leu Leu Glu Ile Asp
                325                 330                 335

Leu Asn Asp Pro Thr Cys Thr Ser Asp Gln Leu Ser Leu Thr Gly Phe
            340                 345                 350

Asn Lys Leu Leu Thr Ala Arg Lys Pro Lys Pro Glu Pro Ser Ile Ile
        355                 360                 365

Ile Glu Thr Ile Leu Pro Ile Asp Pro Asn Tyr Ser Leu Gly Cys Lys
    370                 375                 380

Ser
385
```

<210> 2745
<211> 1345
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1336)
<223> RXA02478

<400> 2745

```
gacatcgtcg aagcgctctc cagcggcaac atcgacgatt atcgcagcgc cgtgctcgct 60

cactacgcgc cgtttcgccg catgatttcc aacatgctcg atg cgc act agc ctc   115
                                              Met Arg Thr Ser Leu
                                                1               5

att gcg cgc ggg ttg tac cgc att ccc gcg ctg gtc tgg gat cag ggt   163
Ile Ala Arg Gly Leu Tyr Arg Ile Pro Ala Leu Val Trp Asp Gln Gly
                10                  15                  20

ctt tta acg ctt ttc gac gcc cgc ctc agt gtt gac gac ctc ccc gca   211
Leu Leu Thr Leu Phe Asp Ala Arg Leu Ser Val Asp Asp Leu Pro Ala
            25                  30                  35

ccc atc gac gtg gtg tca gcg cga tcc tca gac ggc atc acc tgg acc   259
```

```
Pro Ile Asp Val Val Ser Ala Arg Ser Ser Asp Gly Ile Thr Trp Thr
         40                  45                  50

acc cca gaa cca gca atc gtc gaa act gaa cac cgc ggt gtg ggc gat   307
Thr Pro Glu Pro Ala Ile Val Glu Thr Glu His Arg Gly Val Gly Asp
     55                  60                  65

gtc tgc ctt gtc acg ggc gat ctg tgc ttc cac gga ttg tcc aac ctc   355
Val Cys Leu Val Thr Gly Asp Leu Cys Phe His Gly Leu Ser Asn Leu
 70                  75                  80                  85

gca gga ttt ttt gag gat ccc acc gac ctt gaa ccc cgg ctg gcg cgc   403
Ala Gly Phe Phe Glu Asp Pro Thr Asp Leu Glu Pro Arg Leu Ala Arg
                 90                  95                 100

cgg gat gtg agt ggg tgg acg tcg ata agc atg gcc cac tat ttt gcg   451
Arg Asp Val Ser Gly Trp Thr Ser Ile Ser Met Ala His Tyr Phe Ala
            105                 110                 115

gat gtt gat gcc gcg ttc gcc tcg tcg ggg acg gga ctt gtc ctg gcg   499
Asp Val Asp Ala Ala Phe Ala Ser Ser Gly Thr Gly Leu Val Leu Ala
        120                 125                 130

gat ggg cgg tgg att cag agt ttt gtg gtg cgg cgc ggg cgc gag att   547
Asp Gly Arg Trp Ile Gln Ser Phe Val Val Arg Arg Gly Arg Glu Ile
    135                 140                 145

tcg ctt cgg att ctg cgc agc gat ggc cac atc acc gat att gcc ggc   595
Ser Leu Arg Ile Leu Arg Ser Asp Gly His Ile Thr Asp Ile Ala Gly
150                 155                 160                 165

ggt aac gaa tcc gcg atg acg cag ctg ccg agc ggt cgg att gtg ctg   643
Gly Asn Glu Ser Ala Met Thr Gln Leu Pro Ser Gly Arg Ile Val Leu
                170                 175                 180

cat tcc agg ggg gtg gga cac cgt ctg agc agt gtg tcc gat gat ttc   691
His Ser Arg Gly Val Gly His Arg Leu Ser Ser Val Ser Asp Asp Phe
            185                 190                 195

ggg gag aca ttc act ccg ctg gag cct gtg cct gaa cta atc gac ccc   739
Gly Glu Thr Phe Thr Pro Leu Glu Pro Val Pro Glu Leu Ile Asp Pro
        200                 205                 210

ggc tgc aac ggc cac gtg ttc tac tgg aaa gcg gct gga atg ctc gcc   787
Gly Cys Asn Gly His Val Phe Tyr Trp Lys Ala Ala Gly Met Leu Ala
    215                 220                 225

gca acg cac ctg gcg gac cct gat ctg cga cgc cac ttg gtg gtt gat   835
Ala Thr His Leu Ala Asp Pro Asp Leu Arg Arg His Leu Val Val Asp
230                 235                 240                 245

tta tcc agc gac gaa gga gcg acc tgg gcg cat cgc atc acc atc gag   883
Leu Ser Ser Asp Glu Gly Ala Thr Trp Ala His Arg Ile Thr Ile Glu
                250                 255                 260

cgc gaa gaa gcc gcc tat tca acc gct gcg gaa atg ccc aac gga gat   931
Arg Glu Glu Ala Ala Tyr Ser Thr Ala Ala Glu Met Pro Asn Gly Asp
            265                 270                 275

gtt gcc gtg gtg tgg gaa gca gag gga acg cgc gcg ata aaa tgc acg   979
Val Ala Val Val Trp Glu Ala Glu Gly Thr Arg Ala Ile Lys Cys Thr
```

```
        280                 285                 290

gtg atc agc gta aat gat att tcg ctg cgg atc gat gag ccc att tcc   1027
Val Ile Ser Val Asn Asp Ile Ser Leu Arg Ile Asp Glu Pro Ile Ser
    295                 300                 305

gat gcc ata tcc ctc cgc cat gtg gtg atc aac gat gac cat gac ggc   1075
Asp Ala Ile Ser Leu Arg His Val Val Ile Asn Asp Asp His Asp Gly
310                 315                 320                 325

atc gaa gtc gca ctg cct gac gca tcg caa tgg ggt gaa ggt gta ttc   1123
Ile Glu Val Ala Leu Pro Asp Ala Ser Gln Trp Gly Glu Gly Val Phe
                330                 335                 340

aaa att gtg tcc aat cca gac gcg agc acc caa aaa atc cgc act cga   1171
Lys Ile Val Ser Asn Pro Asp Ala Ser Thr Gln Lys Ile Arg Thr Arg
            345                 350                 355

ggc aag ccc gcg cga cag acc ctg gaa att ggg gat gaa ttg gtt ttt   1219
Gly Lys Pro Ala Arg Gln Thr Leu Glu Ile Gly Asp Glu Leu Val Phe
        360                 365                 370

gat atc cgc aag ggt gga gaa gtg gct tac ggc gtc acg gtt cct tat   1267
Asp Ile Arg Lys Gly Gly Glu Val Ala Tyr Gly Val Thr Val Pro Tyr
    375                 380                 385

gat ggt cgc tcg ttg ggg aag tta aac agg att ttg gag tgg ggc tgt   1315
Asp Gly Arg Ser Leu Gly Lys Leu Asn Arg Ile Leu Glu Trp Gly Cys
390                 395                 400                 405

aga ggc cga ttt gcg gtc ctt taattgcgg                            1345
Arg Gly Arg Phe Ala Val Leu
                410
```

Replacement Sheet (Rule 26) RO/AU 12 Jul 2005 11:44:44 PM

<210> 2746
<211> 412
<212> PRT
<213> Corynebacterium glutamicum

<400> 2746

```
Met Arg Thr Ser Leu Ile Ala Arg Gly Leu Tyr Arg Ile Pro Ala Leu
  1               5                  10                  15

Val Trp Asp Gln Gly Leu Leu Thr Leu Phe Asp Ala Arg Leu Ser Val
             20                  25                  30

Asp Asp Leu Pro Ala Pro Ile Asp Val Val Ser Ala Arg Ser Ser Asp
         35                  40                  45

Gly Ile Thr Trp Thr Thr Pro Glu Pro Ala Ile Val Glu Thr Glu His
     50                  55                  60

Arg Gly Val Gly Asp Val Cys Leu Val Thr Gly Asp Leu Cys Phe His
 65                  70                  75                  80

Gly Leu Ser Asn Leu Ala Gly Phe Phe Glu Asp Pro Thr Asp Leu Glu
                 85                  90                  95

Pro Arg Leu Ala Arg Arg Asp Val Ser Gly Trp Thr Ser Ile Ser Met
            100                 105                 110
```

```
Ala His Tyr Phe Ala Asp Val Asp Ala Ala Phe Ala Ser Ser Gly Thr
        115                 120                 125

Gly Leu Val Leu Ala Asp Gly Arg Trp Ile Gln Ser Phe Val Val Arg
    130                 135                 140

Arg Gly Arg Glu Ile Ser Leu Arg Ile Leu Arg Ser Asp Gly His Ile
145                 150                 155                 160

Thr Asp Ile Ala Gly Gly Asn Glu Ser Ala Met Thr Gln Leu Pro Ser
                165                 170                 175

Gly Arg Ile Val Leu His Ser Arg Gly Val Gly His Arg Leu Ser Ser
            180                 185                 190

Val Ser Asp Asp Phe Gly Glu Thr Phe Thr Pro Leu Glu Pro Val Pro
        195                 200                 205

Glu Leu Ile Asp Pro Gly Cys Asn Gly His Val Phe Tyr Trp Lys Ala
    210                 215                 220

Ala Gly Met Leu Ala Ala Thr His Leu Ala Asp Pro Asp Leu Arg Arg
225                 230                 235                 240

His Leu Val Val Asp Leu Ser Ser Asp Glu Gly Ala Thr Trp Ala His
                245                 250                 255

Arg Ile Thr Ile Glu Arg Glu Glu Ala Ala Tyr Ser Thr Ala Ala Glu
            260                 265                 270

Met Pro Asn Gly Asp Val Ala Val Val Trp Glu Ala Glu Gly Thr Arg
        275                 280                 285

Ala Ile Lys Cys Thr Val Ile Ser Val Asn Asp Ile Ser Leu Arg Ile
    290                 295                 300

Asp Glu Pro Ile Ser Asp Ala Ile Ser Leu Arg His Val Val Ile Asn
305                 310                 315                 320

Asp Asp His Asp Gly Ile Glu Val Ala Leu Pro Asp Ala Ser Gln Trp
                325                 330                 335

Gly Glu Gly Val Phe Lys Ile Val Ser Asn Pro Asp Ala Ser Thr Gln
            340                 345                 350

Lys Ile Arg Thr Arg Gly Lys Pro Ala Arg Gln Thr Leu Glu Ile Gly
        355                 360                 365

Asp Glu Leu Val Phe Asp Ile Arg Lys Gly Gly Glu Val Ala Tyr Gly
    370                 375                 380

Val Thr Val Pro Tyr Asp Gly Arg Ser Leu Gly Lys Leu Asn Arg Ile
385                 390                 395                 400

Leu Glu Trp Gly Cys Arg Gly Arg Phe Ala Val Leu
                405                 410
```

<210> 2747
<211> 933

<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(910)
<223> RXA02482

<400> 2747
aaacggtggc gccttaattg ttttacgcgt gctgacagga acctttttagg tgattaacct 60

ggtttgcaac tttccaacct cagccggata aggaacacta gtg ggc gtg gct aaa 115
Val Gly Val Ala Lys
1 5

tca aag aaa tct gct tta cct aaa gtc ctg ctc acc atc gtg gtg atc 163
Ser Lys Lys Ser Ala Leu Pro Lys Val Leu Leu Thr Ile Val Val Ile
10 15 20

ctg ctc ctg ctc gtg ctg gta gca gaa ttc ggg ctg cgc ttc atg atc 211
Leu Leu Leu Leu Val Leu Val Ala Glu Phe Gly Leu Arg Phe Met Ile
25 30 35

gga aaa caa ctg aaa gat gag ttc caa gct cag gct tcc tca caa gga 259
Gly Lys Gln Leu Lys Asp Glu Phe Gln Ala Gln Ala Ser Ser Gln Gly
40 45 50

atc tct gca act gaa gag ccc tcc atc agc ttc ggc gca tcc cca ctc 307
Ile Ser Ala Thr Glu Glu Pro Ser Ile Ser Phe Gly Ala Ser Pro Leu
55 60 65

ctg tta ggc atc gct cgg gga agc atc aat gaa gtc aca atc gac acc 355
Leu Leu Gly Ile Ala Arg Gly Ser Ile Asn Glu Val Thr Ile Asp Thr
70 75 80 85

ccc gac tcc gta tcc atc act aac caa gac ggt gtc ccc tcc atc agt 403
Pro Asp Ser Val Ser Ile Thr Asn Gln Asp Gly Val Pro Ser Ile Ser
90 95 100

ggc aca cca gag tca act atc caa ctc caa ggg ctt gat atc ggt gac 451
Gly Thr Pro Glu Ser Thr Ile Gln Leu Gln Gly Leu Asp Ile Gly Asp
105 110 115

cgc gac aac cca gtc gca gac cac ctc acc tta acc aca ttg gca acc 499
Arg Asp Asn Pro Val Ala Asp His Leu Thr Leu Thr Thr Leu Ala Thr
120 125 130

gac gat ttc atc ctg gca acc atc caa cag cag atg gcc gaa gca acc 547
Asp Asp Phe Ile Leu Ala Thr Ile Gln Gln Gln Met Ala Glu Ala Thr
135 140 145

ggc ggg aac agc acc tcc caa gga ttc gca gaa cag ctt atc cag gaa 595
Gly Gly Asn Ser Thr Ser Gln Gly Phe Ala Glu Gln Leu Ile Gln Glu
150 155 160 165

ctc atc aaa gtc acc gac att act tcc gat gca gct aat caa acc atc 643
Leu Ile Lys Val Thr Asp Ile Thr Ser Asp Ala Ala Asn Gln Thr Ile
170 175 180

gaa gtt gaa ttc acc gac ggc gcc gcc cga gcc tca ctg cac ccc atc 691
Glu Val Glu Phe Thr Asp Gly Ala Ala Arg Ala Ser Leu His Pro Ile

```
            185                 190                 195

gta acg aac ggc caa ctc ggc ttt gag atc gta gat tcc caa ctc ttc   739
Val Thr Asn Gly Gln Leu Gly Phe Glu Ile Val Asp Ser Gln Leu Phe
        200                 205                 210

gga ttc ggc ctc ccc gat gaa atc tcc caa atg ctc acc gac gca ctg   787
Gly Phe Gly Leu Pro Asp Glu Ile Ser Gln Met Leu Thr Asp Ala Leu
    215                 220                 225

caa tca tca atc aat gaa gta gcc ggt ggc ctg caa atc caa agc ctc   835
Gln Ser Ser Ile Asn Glu Val Ala Gly Gly Leu Gln Ile Gln Ser Leu
230                 235                 240                 245

gaa gtt gtc gac gct ggc atc aac gtc acc ctg acc gga gac aac atc   883
Glu Val Val Asp Ala Gly Ile Asn Val Thr Leu Thr Gly Asp Asn Ile
                250                 255                 260

aac atc cag acc cta gaa gcc gca cag taaagagcgc tttcgcgtct         930
Asn Ile Gln Thr Leu Glu Ala Ala Gln
            265                 270

gtg                                                              933


<210> 2748
<211> 270
<212> PRT
<213> Corynebacterium glutamicum

<400> 2748
Val Gly Val Ala Lys Ser Lys Lys Ser Ala Leu Pro Lys Val Leu Leu
  1               5                  10                  15

Thr Ile Val Val Ile Leu Leu Leu Leu Val Leu Val Ala Glu Phe Gly
             20                  25                  30

Leu Arg Phe Met Ile Gly Lys Gln Leu Lys Asp Glu Phe Gln Ala Gln
         35                  40                  45

Ala Ser Ser Gln Gly Ile Ser Ala Thr Glu Glu Pro Ser Ile Ser Phe
     50                  55                  60

Gly Ala Ser Pro Leu Leu Leu Gly Ile Ala Arg Gly Ser Ile Asn Glu
 65                  70                  75                  80

Val Thr Ile Asp Thr Pro Asp Ser Val Ser Ile Thr Asn Gln Asp Gly
                 85                  90                  95

Val Pro Ser Ile Ser Gly Thr Pro Glu Ser Thr Ile Gln Leu Gln Gly
            100                 105                 110

Leu Asp Ile Gly Asp Arg Asp Asn Pro Val Ala Asp His Leu Thr Leu
        115                 120                 125

Thr Thr Leu Ala Thr Asp Asp Phe Ile Leu Ala Thr Ile Gln Gln Gln
    130                 135                 140

Met Ala Glu Ala Thr Gly Gly Asn Ser Thr Ser Gln Gly Phe Ala Glu
145                 150                 155                 160
```

```
Gln Leu Ile Gln Glu Leu Ile Lys Val Thr Asp Ile Thr Ser Asp Ala
                165                 170                 175

Ala Asn Gln Thr Ile Glu Val Glu Phe Thr Asp Gly Ala Ala Arg Ala
            180                 185                 190

Ser Leu His Pro Ile Val Thr Asn Gly Gln Leu Gly Phe Glu Ile Val
        195                 200                 205

Asp Ser Gln Leu Phe Gly Phe Gly Leu Pro Asp Glu Ile Ser Gln Met
    210                 215                 220

Leu Thr Asp Ala Leu Gln Ser Ser Ile Asn Glu Val Ala Gly Gly Leu
225                 230                 235                 240

Gln Ile Gln Ser Leu Glu Val Val Asp Ala Gly Ile Asn Val Thr Leu
                245                 250                 255

Thr Gly Asp Asn Ile Asn Ile Gln Thr Leu Glu Ala Ala Gln
            260                 265                 270


<210> 2749
<211> 936
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(913)
<223> RXA02483

<400> 2749
catgggccct gcaatcgagc ctaaggttgc cgacgcactc ggcgagctct tcgcaaacga 60

aggcgctctg accgaaaagt ggatctccga gaacctctaa atg gct gat cac gcc   115
                                              Met Ala Asp His Ala
                                                1               5

cac aat ctg cgc gcc tct ttc cgc aag ggt gca aac gga aag cag aag   163
His Asn Leu Arg Ala Ser Phe Arg Lys Gly Ala Asn Gly Lys Gln Lys
                10                  15                  20

cca atc ggc gtg atc acc cgc ggc acc acc ggt gtg aac cgc cta cgg   211
Pro Ile Gly Val Ile Thr Arg Gly Thr Thr Gly Val Asn Arg Leu Arg
            25                  30                  35

cgc ttc gat cgg tgg tgc ttt cat cat ccc aaa ata cgt tcg ctt ctc   259
Arg Phe Asp Arg Trp Cys Phe His His Pro Lys Ile Arg Ser Leu Leu
        40                  45                  50

gac gcc act tcc ctg gcg tta gat gtc ggg tac ggc gcc agc cac aca   307
Asp Ala Thr Ser Leu Ala Leu Asp Val Gly Tyr Gly Ala Ser His Thr
    55                  60                  65

acc acc gtc gaa tgg gga cgt tgg ctc cac cgc ctc caa ccc gac atg   355
Thr Thr Val Glu Trp Gly Arg Trp Leu His Arg Leu Gln Pro Asp Met
70                  75                  80                  85

gat gtc atc ggc cta gaa atc aac ccc gaa cga gtc ctc gaa ccc caa   403
Asp Val Ile Gly Leu Glu Ile Asn Pro Glu Arg Val Leu Glu Pro Gln
```

```
                90                  95                 100

aac ggc gtg tcc ttt gaa ctc ggc gga ttc gaa ctt gcc ggc tac acc   451
Asn Gly Val Ser Phe Glu Leu Gly Gly Phe Glu Leu Ala Gly Tyr Thr
            105                 110                 115

cca caa ctc gtg cgc gcc ttc aac gtg ctg cgc caa tac gac gtg gac   499
Pro Gln Leu Val Arg Ala Phe Asn Val Leu Arg Gln Tyr Asp Val Asp
        120                 125                 130

caa gtc gaa gcc gca tgg gaa acc gtc acc tcc aga ctt gcc cca ggc   547
Gln Val Glu Ala Ala Trp Glu Thr Val Thr Ser Arg Leu Ala Pro Gly
    135                 140                 145

gga ctg ttt ttc gaa ggc acc tgc gat gaa atc ggc aaa cgc tgc acc   595
Gly Leu Phe Phe Glu Gly Thr Cys Asp Glu Ile Gly Lys Arg Cys Thr
150                 155                 160                 165

tgg atc aca ctt aac tca gac ggc cca caa gaa ctc acc ctt gca tgg   643
Trp Ile Thr Leu Asn Ser Asp Gly Pro Gln Glu Leu Thr Leu Ala Trp
                170                 175                 180

gat cct tgg gga atc tcc acc ccc tcc gat gtg gcc gaa cga ctg ccc   691
Asp Pro Trp Gly Ile Ser Thr Pro Ser Asp Val Ala Glu Arg Leu Pro
            185                 190                 195

aaa atg ctc atc cac cgc aac att cct ggt gaa aag att cac gca ctg   739
Lys Met Leu Ile His Arg Asn Ile Pro Gly Glu Lys Ile His Ala Leu
        200                 205                 210

cta gca gcc gct gat tta gcc tgg gac tac tgc gcc ggc tgg gaa ccc   787
Leu Ala Ala Ala Asp Leu Ala Trp Asp Tyr Cys Ala Gly Trp Glu Pro
    215                 220                 225

cac gga ccg cgc gtg cgc tgg gaa aaa gcc cgc gag atg ctc atc gac   835
His Gly Pro Arg Val Arg Trp Glu Lys Ala Arg Glu Met Leu Ile Asp
230                 235                 240                 245

caa ggt tgg ccc atc gca gtg tcc agg cga cgc gtg ggc gat agc ctg   883
Gln Gly Trp Pro Ile Ala Val Ser Arg Arg Arg Val Gly Asp Ser Leu
                250                 255                 260

ctg act gta ccg tgg gaa acg gtg gcg cct taattgtttt acgcgtgctg     933
Leu Thr Val Pro Trp Glu Thr Val Ala Pro
            265                 270

aca                                                               936


<210> 2750
<211> 271
<212> PRT
<213> Corynebacterium glutamicum

<400> 2750
Met Ala Asp His Ala His Asn Leu Arg Ala Ser Phe Arg Lys Gly Ala
  1               5                  10                  15

Asn Gly Lys Gln Lys Pro Ile Gly Val Ile Thr Arg Gly Thr Thr Gly
             20                  25                  30
```

```
Val Asn Arg Leu Arg Arg Phe Asp Arg Trp Cys Phe His His Pro Lys
          35                  40                  45

Ile Arg Ser Leu Leu Asp Ala Thr Ser Leu Ala Leu Asp Val Gly Tyr
      50                  55                  60

Gly Ala Ser His Thr Thr Thr Val Glu Trp Gly Arg Trp Leu His Arg
 65                  70                  75                  80

Leu Gln Pro Asp Met Asp Val Ile Gly Leu Glu Ile Asn Pro Glu Arg
                 85                  90                  95

Val Leu Glu Pro Gln Asn Gly Val Ser Phe Glu Leu Gly Gly Phe Glu
            100                 105                 110

Leu Ala Gly Tyr Thr Pro Gln Leu Val Arg Ala Phe Asn Val Leu Arg
        115                 120                 125

Gln Tyr Asp Val Asp Gln Val Glu Ala Ala Trp Glu Thr Val Thr Ser
    130                 135                 140

Arg Leu Ala Pro Gly Gly Leu Phe Phe Glu Gly Thr Cys Asp Glu Ile
145                 150                 155                 160

Gly Lys Arg Cys Thr Trp Ile Thr Leu Asn Ser Asp Gly Pro Gln Glu
                165                 170                 175

Leu Thr Leu Ala Trp Asp Pro Trp Gly Ile Ser Thr Pro Ser Asp Val
            180                 185                 190

Ala Glu Arg Leu Pro Lys Met Leu Ile His Arg Asn Ile Pro Gly Glu
        195                 200                 205

Lys Ile His Ala Leu Leu Ala Ala Ala Asp Leu Ala Trp Asp Tyr Cys
    210                 215                 220

Ala Gly Trp Glu Pro His Gly Pro Arg Val Arg Trp Glu Lys Ala Arg
225                 230                 235                 240

Glu Met Leu Ile Asp Gln Gly Trp Pro Ile Ala Val Ser Arg Arg Arg
                245                 250                 255

Val Gly Asp Ser Leu Leu Thr Val Pro Trp Glu Thr Val Ala Pro
            260                 265                 270


<210> 2751
<211> 624
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(601)
<223> RXA02484

<400> 2751
cggcgaaagt gacttccgaa tcgagttcga cgccgtcgat cgcggcgatt tcctgggcta 60

gcgatgaatc caacacccca ctaacggtag tcttatcctc atg gca acg cgt aca   115
                                              Met Ala Thr Arg Thr
```

```
                                                    1               5

gaa aac acc att acg atc aat cag ccc gtc ggc aag gtg cac caa gca   163
Glu Asn Thr Ile Thr Ile Asn Gln Pro Val Gly Lys Val His Gln Ala
                 10                  15                  20

ctg acc acc gaa gcc tac tgg gca tac atc gca gag aac ctc tcc ccc   211
Leu Thr Thr Glu Ala Tyr Trp Ala Tyr Ile Ala Glu Asn Leu Ser Pro
             25                  30                  35

gaa gct ggc gag gtc aac gag ttc acc gca gct gac ggt ggc gca acc   259
Glu Ala Gly Glu Val Asn Glu Phe Thr Ala Ala Asp Gly Gly Ala Thr
         40                  45                  50

gca acc ctt ttt gag gtc ctc cca ctc gag gtc ctc cca gag gca gtt   307
Ala Thr Leu Phe Glu Val Leu Pro Leu Glu Val Leu Pro Glu Ala Val
     55                  60                  65

cgc gca atg atc agc cag gca ctg aag gtc aag cga gtc ctc acg gtt   355
Arg Ala Met Ile Ser Gln Ala Leu Lys Val Lys Arg Val Leu Thr Val
 70                  75                  80                  85

cct gca ctg acc aac aac gcc aca acc gtc gag tac aac gct gac gtc   403
Pro Ala Leu Thr Asn Asn Ala Thr Thr Val Glu Tyr Asn Ala Asp Val
                 90                  95                 100

aag ggc acc cct gtt gat ttc aag ggc acc atc gcc atc aac ggc gac   451
Lys Gly Thr Pro Val Asp Phe Lys Gly Thr Ile Ala Ile Asn Gly Asp
             105                 110                 115

gac gca gca acc acc ttc gac tac agc aac gaa gtg tcc gtg aac atc   499
Asp Ala Ala Thr Thr Phe Asp Tyr Ser Asn Glu Val Ser Val Asn Ile
         120                 125                 130

cca ttc atg ggc cct gca atc gag cct aag gtt gcc gac gca ctc ggc   547
Pro Phe Met Gly Pro Ala Ile Glu Pro Lys Val Ala Asp Ala Leu Gly
    135                 140                 145

gag ctc ttc gca aac gaa ggc gct ctg acc gaa aag tgg atc tcc gag   595
Glu Leu Phe Ala Asn Glu Gly Ala Leu Thr Glu Lys Trp Ile Ser Glu
150                 155                 160                 165

aac ctc taaatggctg atcacgccca caa                                624
Asn Leu
```

<210> 2752
<211> 167
<212> PRT
<213> Corynebacterium glutamicum

<400> 2752

```
Met Ala Thr Arg Thr Glu Asn Thr Ile Thr Ile Asn Gln Pro Val Gly
  1               5                  10                  15

Lys Val His Gln Ala Leu Thr Thr Glu Ala Tyr Trp Ala Tyr Ile Ala
             20                  25                  30

Glu Asn Leu Ser Pro Glu Ala Gly Glu Val Asn Glu Phe Thr Ala Ala
         35                  40                  45
```

```
Asp Gly Gly Ala Thr Ala Thr Leu Phe Glu Val Leu Pro Leu Glu Val
     50                  55                  60

Leu Pro Glu Ala Val Arg Ala Met Ile Ser Gln Ala Leu Lys Val Lys
 65                  70                  75                  80

Arg Val Leu Thr Val Pro Ala Leu Thr Asn Asn Ala Thr Thr Val Glu
                 85                  90                  95

Tyr Asn Ala Asp Val Lys Gly Thr Pro Val Asp Phe Lys Gly Thr Ile
            100                 105                 110

Ala Ile Asn Gly Asp Asp Ala Ala Thr Thr Phe Asp Tyr Ser Asn Glu
        115                 120                 125

Val Ser Val Asn Ile Pro Phe Met Gly Pro Ala Ile Glu Pro Lys Val
    130                 135                 140

Ala Asp Ala Leu Gly Glu Leu Phe Ala Asn Glu Gly Ala Leu Thr Glu
145                 150                 155                 160

Lys Trp Ile Ser Glu Asn Leu
                165
```

<210> 2753
<211> 759
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(736)
<223> RXA02486

<400> 2753

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tccgacctcg tcgcattagc caaagaaatc cgcgacggag tcctcgaaac cttcggcgtc 60

accctcgtcc cagaacccgt ctggattgga atcagcatcg atg act gaa ttt tcc   115
                                              Met Thr Glu Phe Ser
                                                1               5

gac gtc cct ggc acc gcc gcc cca ctg cac agg gcg ttg gaa aat gcc   163
Asp Val Pro Gly Thr Ala Ala Pro Leu His Arg Ala Leu Glu Asn Ala
                 10                  15                  20

gga tac tcc act tta gaa tcc ctc gac ggt gtt ccc tac aag acg ttg   211
Gly Tyr Ser Thr Leu Glu Ser Leu Asp Gly Val Pro Tyr Lys Thr Leu
             25                  30                  35

att gcc ctg cat ggt gtc gga aaa act ggc ctc ggc agg atc cag gca   259
Ile Ala Leu His Gly Val Gly Lys Thr Gly Leu Gly Arg Ile Gln Ala
         40                  45                  50

gca ttg ttg gaa cgt ggc ctt tcc ctg ggg gaa gaa aca aaa ggc gcc   307
Ala Leu Leu Glu Arg Gly Leu Ser Leu Gly Glu Glu Thr Lys Gly Ala
     55                  60                  65

acc atc acc cca ggt cac acc ggt aaa gtg gcc tca gat atc aaa act   355
Thr Ile Thr Pro Gly His Thr Gly Lys Val Ala Ser Asp Ile Lys Thr
```

```
 70                  75                  80                  85

cac atc act tcc gtg gat ccc gtc gca tac gtc gat ggt cta gag ggg   403
His Ile Thr Ser Val Asp Pro Val Ala Tyr Val Asp Gly Leu Glu Gly
                 90                  95                 100

cgt cgg gtt gct cac ggg cac caa ttg cta tcg atc ttc ggt cgc gtc   451
Arg Arg Val Ala His Gly His Gln Leu Leu Ser Ile Phe Gly Arg Val
            105                 110                 115

acc ggc gcg gaa ccc aaa atg tgg gga ccc tcc atg atc gga tac ggc   499
Thr Gly Ala Glu Pro Lys Met Trp Gly Pro Ser Met Ile Gly Tyr Gly
        120                 125                 130

tca gtc cac tac gtt tcc cac acc gga agg gaa ggc gat tgg ttt cag   547
Ser Val His Tyr Val Ser His Thr Gly Arg Glu Gly Asp Trp Phe Gln
    135                 140                 145

tgt ggt ttc agc ccg gcg aag tcc aaa atc tgc ctg tat ggc ctg aag   595
Cys Gly Phe Ser Pro Ala Lys Ser Lys Ile Cys Leu Tyr Gly Leu Lys
150                 155                 160                 165

gat tcg cct cgc ggt gag gaa ttg ctg cag aaa ctt gga aaa tac acc   643
Asp Ser Pro Arg Gly Glu Glu Leu Leu Gln Lys Leu Gly Lys Tyr Thr
                170                 175                 180

gaa ggc cgc gga tgc gtg tac atc aat aaa ccg gaa gac atc gat ttg   691
Glu Gly Arg Gly Cys Val Tyr Ile Asn Lys Pro Glu Asp Ile Asp Leu
            185                 190                 195

gat gtt tta gag gcc atg atc agc gag tca tgg gcc ggc caa ggc       736
Asp Val Leu Glu Ala Met Ile Ser Glu Ser Trp Ala Gly Gln Gly
        200                 205                 210

taggttgcaa atccccacca caa                                        759


<210> 2754
<211> 212
<212> PRT
<213> Corynebacterium glutamicum

<400> 2754
Met Thr Glu Phe Ser Asp Val Pro Gly Thr Ala Ala Pro Leu His Arg
  1               5                  10                  15

Ala Leu Glu Asn Ala Gly Tyr Ser Thr Leu Glu Ser Leu Asp Gly Val
             20                  25                  30

Pro Tyr Lys Thr Leu Ile Ala Leu His Gly Val Gly Lys Thr Gly Leu
         35                  40                  45

Gly Arg Ile Gln Ala Ala Leu Leu Glu Arg Gly Leu Ser Leu Gly Glu
     50                  55                  60

Glu Thr Lys Gly Ala Thr Ile Thr Pro Gly His Thr Gly Lys Val Ala
 65                  70                  75                  80

Ser Asp Ile Lys Thr His Ile Thr Ser Val Asp Pro Val Ala Tyr Val
                 85                  90                  95
```

```
Asp Gly Leu Glu Gly Arg Arg Val Ala His Gly His Gln Leu Leu Ser
            100                 105                 110

Ile Phe Gly Arg Val Thr Gly Ala Glu Pro Lys Met Trp Gly Pro Ser
        115                 120                 125

Met Ile Gly Tyr Gly Ser Val His Tyr Val Ser His Thr Gly Arg Glu
    130                 135                 140

Gly Asp Trp Phe Gln Cys Gly Phe Ser Pro Ala Lys Ser Lys Ile Cys
145                 150                 155                 160

Leu Tyr Gly Leu Lys Asp Ser Pro Arg Gly Glu Glu Leu Leu Gln Lys
                165                 170                 175

Leu Gly Lys Tyr Thr Glu Gly Arg Gly Cys Val Tyr Ile Asn Lys Pro
            180                 185                 190

Glu Asp Ile Asp Leu Asp Val Leu Glu Ala Met Ile Ser Glu Ser Trp
        195                 200                 205

Ala Gly Gln Gly
    210
```

Sequence Listing_ST25.txt

<210> 2755
<211> 392
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(369)
<223> RXA02488

<400> 2755

```
aag ctg act gca act ggt gtc gat gtc atg ggc acc ttc tac cca gaa   48
Lys Leu Thr Ala Thr Gly Val Asp Val Met Gly Thr Phe Tyr Pro Glu
  1               5                  10                  15

ggt gaa gca ctt gcg cca atc act ttg aac ctc acc aac gaa gtt gta   96
Gly Glu Ala Leu Ala Pro Ile Thr Leu Asn Leu Thr Asn Glu Val Val
             20                  25                  30

tgc gac gag cct gaa acc ccc gtt gag cct gag gtt cct gta gag cct   144
Cys Asp Glu Pro Glu Thr Pro Val Glu Pro Glu Val Pro Val Glu Pro
         35                  40                  45

gag act cca gta gat ccg gaa acc tcg gtc gac cca gag act cca gta   192
Glu Thr Pro Val Asp Pro Glu Thr Ser Val Asp Pro Glu Thr Pro Val
     50                  55                  60

gat ccg gaa acc tcg gtc gac cca gaa aag cct ggc gat gac aac aag   240
Asp Pro Glu Thr Ser Val Asp Pro Glu Lys Pro Gly Asp Asp Asn Lys
 65                  70                  75                  80

gat gac gga agc aac agc agc agc aac ggc gat atc ctc gga atc ttg   288
Asp Asp Gly Ser Asn Ser Ser Ser Asn Gly Asp Ile Leu Gly Ile Leu
                 85                  90                  95

ggc atc ctc gca gcg ctt ggt ggc gtt ggt gca ctt gtg tac aac ttc   336
```

```
Gly Ile Leu Ala Ala Leu Gly Gly Val Gly Ala Leu Val Tyr Asn Phe
            100                 105                 110

ctg gta gct agc gga ttc ctt gca gcg ttt aag taaatgaatc gttttcctag 389
Leu Val Ala Ser Gly Phe Leu Ala Ala Phe Lys
        115                 120

tgc                                                               392


<210> 2756
<211> 123
<212> PRT
<213> Corynebacterium glutamicum

<400> 2756
Lys Leu Thr Ala Thr Gly Val Asp Val Met Gly Thr Phe Tyr Pro Glu
  1               5                  10                  15

Gly Glu Ala Leu Ala Pro Ile Thr Leu Asn Leu Thr Asn Glu Val Val
             20                  25                  30

Cys Asp Glu Pro Glu Thr Pro Val Glu Pro Glu Val Pro Val Glu Pro
         35                  40                  45

Glu Thr Pro Val Asp Pro Glu Thr Ser Val Asp Pro Glu Thr Pro Val
     50                  55                  60

Asp Pro Glu Thr Ser Val Asp Pro Glu Lys Pro Gly Asp Asp Asn Lys
 65                  70                  75                  80

Asp Asp Gly Ser Asn Ser Ser Ser Asn Gly Asp Ile Leu Gly Ile Leu
                 85                  90                  95

Gly Ile Leu Ala Ala Leu Gly Gly Val Gly Ala Leu Val Tyr Asn Phe
            100                 105                 110

Leu Val Ala Ser Gly Phe Leu Ala Ala Phe Lys
        115                 120


<210> 2757
<211> 724
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(724)
<223> RXA02489

<400> 2757
tatcctcgga atcttgggca tcctcgcagc gcttggtggc gttggtgcac ttgtgtacaa 60

cttcctggta gctagcggat tccttgcagc gtttaagtaa atg aat cgt ttt cct   115
                                               Met Asn Arg Phe Pro
                                                 1               5

agt gcc tta tta gca gcc tct gtc gcg ggg gct gcg ttg gcc att cca   163
Ser Ala Leu Leu Ala Ala Ser Val Ala Gly Ala Ala Leu Ala Ile Pro
                10                  15                  20
```

```
gcg acc tct gca cat gca gca gaa tct att tgt aca ttc acc ggc gat   211
Ala Thr Ser Ala His Ala Ala Glu Ser Ile Cys Thr Phe Thr Gly Asp
             25                  30                  35

gtt ggg tgg aat gtg cgc gat tct ttc aac agt tat ctt ttg gga aac   259
Val Gly Trp Asn Val Arg Asp Ser Phe Asn Ser Tyr Leu Leu Gly Asn
         40                  45                  50

atc gca aat ggt agt gct tat aaa tat aag ggc ggg ttg gac gtt cgt   307
Ile Ala Asn Gly Ser Ala Tyr Lys Tyr Lys Gly Gly Leu Asp Val Arg
     55                  60                  65

gac ggc gtc cag acc gac ggt aac ggc aaa act cca gca ctg acc tgg   355
Asp Gly Val Gln Thr Asp Gly Asn Gly Lys Thr Pro Ala Leu Thr Trp
 70                  75                  80                  85

cca gtt gat tcg gtg acg tct tcg aag att tcc act tcc gga ggc gcg   403
Pro Val Asp Ser Val Thr Ser Ser Lys Ile Ser Thr Ser Gly Gly Ala
                 90                  95                 100

cac tgg acc gga cac aac ctg tac ccc ggt gat gac ctc gcg gaa gtc   451
His Trp Thr Gly His Asn Leu Tyr Pro Gly Asp Asp Leu Ala Glu Val
            105                 110                 115

cct aac aat ttc acg ttg gat ctt gat ttt tcc aac atc act gtg gag   499
Pro Asn Asn Phe Thr Leu Asp Leu Asp Phe Ser Asn Ile Thr Val Glu
        120                 125                 130

ctg agt ggt tct aca ggt cgg ttg ttg gtg gat tac aca tct cgg gaa   547
Leu Ser Gly Ser Thr Gly Arg Leu Leu Val Asp Tyr Thr Ser Arg Glu
    135                 140                 145

tac atc aac acc cac acg ttg ggt gag ttt caa act ggt gaa cag gct   595
Tyr Ile Asn Thr His Thr Leu Gly Glu Phe Gln Thr Gly Glu Gln Ala
150                 155                 160                 165

gag ctt gcc acg att act ttt gcc aaa gct cca gac ctc acc tct aat   643
Glu Leu Ala Thr Ile Thr Phe Ala Lys Ala Pro Asp Leu Thr Ser Asn
                170                 175                 180

tca gtc aac gtg act ggc gat gtg gca ttg act gct gat ggt gtg gaa   691
Ser Val Asn Val Thr Gly Asp Val Ala Leu Thr Ala Asp Gly Val Glu
            185                 190                 195

gtt ttc ggt ggt ttc tac acg gca ggg gag gag                      724
Val Phe Gly Gly Phe Tyr Thr Ala Gly Glu Glu
        200                 205
```

<210> 2758
<211> 208
<212> PRT
<213> Corynebacterium glutamicum

<400> 2758

```
Met Asn Arg Phe Pro Ser Ala Leu Leu Ala Ala Ser Val Ala Gly Ala
  1               5                  10                  15

Ala Leu Ala Ile Pro Ala Thr Ser Ala His Ala Ala Glu Ser Ile Cys
             20                  25                  30
```

```
Thr Phe Thr Gly Asp Val Gly Trp Asn Val Arg Asp Ser Phe Asn Ser
         35                  40                  45

Tyr Leu Leu Gly Asn Ile Ala Asn Gly Ser Ala Tyr Lys Tyr Lys Gly
     50                  55                  60

Gly Leu Asp Val Arg Asp Gly Val Gln Thr Asp Gly Asn Gly Lys Thr
 65                  70                  75                  80

Pro Ala Leu Thr Trp Pro Val Asp Ser Val Thr Ser Ser Lys Ile Ser
                 85                  90                  95

Thr Ser Gly Gly Ala His Trp Thr Gly His Asn Leu Tyr Pro Gly Asp
            100                 105                 110

Asp Leu Ala Glu Val Pro Asn Asn Phe Thr Leu Asp Leu Asp Phe Ser
        115                 120                 125

Asn Ile Thr Val Glu Leu Ser Gly Ser Thr Gly Arg Leu Leu Val Asp
    130                 135                 140

Tyr Thr Ser Arg Glu Tyr Ile Asn Thr His Thr Leu Gly Glu Phe Gln
145                 150                 155                 160

Thr Gly Glu Gln Ala Glu Leu Ala Thr Ile Thr Phe Ala Lys Ala Pro
                165                 170                 175

Asp Leu Thr Ser Asn Ser Val Asn Val Thr Gly Asp Val Ala Leu Thr
            180                 185                 190

Ala Asp Gly Val Glu Val Phe Gly Gly Phe Tyr Thr Ala Gly Glu Glu
        195                 200                 205
```

DO NOT ENTER

<210> 2759
<211> 2691
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2668)
<223> RXA02495

<400> 2759

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aaggaggaaa attatcaccg tcttaaaaac ggctaaggct tttctaaatt cgccgctgcg 60

caccatcacg tggcgcagcg ttgtggcgaa taaactccgc atg gca tta aca gtg   115
                                          Met Ala Leu Thr Val
                                            1               5

ctt tcg gtt gtg cta gga acc gca ttt ttg tgt ggc tcc ctc ctc ctc   163
Leu Ser Val Val Leu Gly Thr Ala Phe Leu Cys Gly Ser Leu Leu Leu
                10                  15                  20

aca cat tcc ctt gaa aga aca ttt tcc tcc atc gtt gat gcc ggc gtg   211
Thr His Ser Leu Glu Arg Thr Phe Ser Ser Ile Val Asp Ala Gly Val
```

```
                25                  30                  35

gag ggc gtt gac gtg ggc gtt atc gcg caa caa aac aac ccc gac ggc   259
Glu Gly Val Asp Val Gly Val Ile Ala Gln Gln Asn Asn Pro Asp Gly
          40                  45                  50

gta cct ttc tcc gtc atc gcc gaa att gag cag tat ccg gaa gtc cgc   307
Val Pro Phe Ser Val Ile Ala Glu Ile Glu Gln Tyr Pro Glu Val Arg
     55                  60                  65

gcc gtc aac atc atc ggc gac ggc ccc ggc atg ccc tcc ggc acc acc   355
Ala Val Asn Ile Ile Gly Asp Gly Pro Gly Met Pro Ser Gly Thr Thr
 70                  75                  80                  85

atg acc ggc caa tcc gcg ctg atc ctc acc gac tcc gac ggc aat ccc   403
Met Thr Gly Gln Ser Ala Leu Ile Leu Thr Asp Ser Asp Gly Asn Pro
                 90                  95                 100

ctg caa gca ggc agc tcc ggc acg cac ccg cta gcc att tat ccg cag   451
Leu Gln Ala Gly Ser Ser Gly Thr His Pro Leu Ala Ile Tyr Pro Gln
            105                 110                 115

ggc gag tgg gtc tcg ccc gag cca acg ctt atc gac ggc cac ttc ccc   499
Gly Glu Trp Val Ser Pro Glu Pro Thr Leu Ile Asp Gly His Phe Pro
        120                 125                 130

aca aaa ccc gac gag gta gta gtc aac gct tcg gcc gcc aaa cgt ggc   547
Thr Lys Pro Asp Glu Val Val Val Asn Ala Ser Ala Ala Lys Arg Gly
    135                 140                 145

ggg ctc tcc ctc ggt gat cac cta acg atc gtc aca ccc acc gaa cgc   595
Gly Leu Ser Leu Gly Asp His Leu Thr Ile Val Thr Pro Thr Glu Arg
150                 155                 160                 165

atc gac gcc acc ctg tct gga acc ttc gaa tca aac acc gac gtc gca   643
Ile Asp Ala Thr Leu Ser Gly Thr Phe Glu Ser Asn Thr Asp Val Ala
                170                 175                 180

ggc tgg gtc gga gtc gga ttc acc cca cag cgc tac gtc gaa ctg ctc   691
Gly Trp Val Gly Val Gly Phe Thr Pro Gln Arg Tyr Val Glu Leu Leu
            185                 190                 195

acc aac ggc acc gac gcc agc caa atc acc atc gca gtc aac gac ggc   739
Thr Asn Gly Thr Asp Ala Ser Gln Ile Thr Ile Ala Val Asn Asp Gly
        200                 205                 210

gcc gac ccc atg gca gtc cgc aac cgc atc ggc aaa aac cac cgg gac   787
Ala Asp Pro Met Ala Val Arg Asn Arg Ile Gly Lys Asn His Arg Asp
    215                 220                 225

ctg ctg ccc ctg ctg ccc gag caa atc atc gac caa acc acc ggc gac   835
Leu Leu Pro Leu Leu Pro Glu Gln Ile Ile Asp Gln Thr Thr Gly Asp
230                 235                 240                 245

acc gac cgc caa ctg gag ttc atg acc tac gtg ctc ctg gca ttc gcc   883
Thr Asp Arg Gln Leu Glu Phe Met Thr Tyr Val Leu Leu Ala Phe Ala
                250                 255                 260

gcg atc gca ctg att gtt ggc tcg ttc atc att gcc aac acc ttc gcg   931
Ala Ile Ala Leu Ile Val Gly Ser Phe Ile Ile Ala Asn Thr Phe Ala
            265                 270                 275
```

```
atg atc gtc gcc caa cgc acc ggc gaa ttc gcc ctc ctc cgt tcc att   979
Met Ile Val Ala Gln Arg Thr Gly Glu Phe Ala Leu Leu Arg Ser Ile
        280                 285                 290

ggt gtc tcc acg ttc caa atc gga ttc tcc gtg att atg gaa gca gta   1027
Gly Val Ser Thr Phe Gln Ile Gly Phe Ser Val Ile Met Glu Ala Val
    295                 300                 305

ttc gtc gga ctt atc ggc ggt ttc atc ggc atc gca gtt ggc ttc gga   1075
Phe Val Gly Leu Ile Gly Gly Phe Ile Gly Ile Ala Val Gly Phe Gly
310                 315                 320                 325

gtg gtc aat gca ctt gtc caa gtg ctc aac caa ttc ggc gac acc ctc   1123
Val Val Asn Ala Leu Val Gln Val Leu Asn Gln Phe Gly Asp Thr Leu
                330                 335                 340

tcc tcc atc gac atc acc tac aac gcc gga tcc ttc atc ttc cct gtc   1171
Ser Ser Ile Asp Ile Thr Tyr Asn Ala Gly Ser Phe Ile Phe Pro Val
            345                 350                 355

ctc ttc gcc gtc act gcc acc gta cta agc tcc ata tcg cct gct cac   1219
Leu Phe Ala Val Thr Ala Thr Val Leu Ser Ser Ile Ser Pro Ala His
        360                 365                 370

cgc gcc ggt aac ctc cca cca gtc caa gca ttc gaa tcc tcc gat gca   1267
Arg Ala Gly Asn Leu Pro Pro Val Gln Ala Phe Glu Ser Ser Asp Ala
    375                 380                 385

cgc agc gac gcc ctc gga agg atc cgc ttc ctc gtc gcc gcc gtc atg   1315
Arg Ser Asp Ala Leu Gly Arg Ile Arg Phe Leu Val Ala Ala Val Met
390                 395                 400                 405

ctc acc ctt gga atc agc ctg acg atc gca ggt gcc gtg gta tcc gcc   1363
Leu Thr Leu Gly Ile Ser Leu Thr Ile Ala Gly Ala Val Val Ser Ala
                410                 415                 420

atc aac gga gat gaa ttc aaa aca gaa aca cgc ctc gca ttc atc ggc   1411
Ile Asn Gly Asp Glu Phe Lys Thr Glu Thr Arg Leu Ala Phe Ile Gly
            425                 430                 435

gct gga ctt ctc tta gtg ttc ttc tca ctc tcc ctg tcc ggt ccc gca   1459
Ala Gly Leu Leu Leu Val Phe Phe Ser Leu Ser Leu Ser Gly Pro Ala
        440                 445                 450

ctg atg gtg gcg acc tct cag act ctt ggc gtg gcg ata atg tcg ccg   1507
Leu Met Val Ala Thr Ser Gln Thr Leu Gly Val Ala Ile Met Ser Pro
    455                 460                 465

ttc cga gcc gtc ggc aag ctc gca caa cgc aac acc ctg cgc aat ccg   1555
Phe Arg Ala Val Gly Lys Leu Ala Gln Arg Asn Thr Leu Arg Asn Pro
470                 475                 480                 485

cga cgc tcc gca acc acc gca ctg gcc gtc act ttg agc gtt ggc ctc   1603
Arg Arg Ser Ala Thr Thr Ala Leu Ala Val Thr Leu Ser Val Gly Leu
                490                 495                 500

gtc gcc tgc gtt gga gtc atc ggc gcc acc acc cgc gcc agc gtc ttc   1651
Val Ala Cys Val Gly Val Ile Gly Ala Thr Thr Arg Ala Ser Val Phe
            505                 510                 515
```

```
ggg tcc atg gaa tcc acc atc aaa tcc cca tat gtc ctc gac agc atc   1699
Gly Ser Met Glu Ser Thr Ile Lys Ser Pro Tyr Val Leu Asp Ser Ile
        520                 525                 530

ggt ggc acc atg atc cct gga caa ccc gcc ggc ggt tca agg tca ctg   1747
Gly Gly Thr Met Ile Pro Gly Gln Pro Ala Gly Gly Ser Arg Ser Leu
    535                 540                 545

tcc atg tcc gca gcc gtc gca cag gaa atc gca caa acc cgc gga gtc   1795
Ser Met Ser Ala Ala Val Ala Gln Glu Ile Ala Gln Thr Arg Gly Val
550                 555                 560                 565

ggc aaa gtg ggc acc ctc atg acc ggc agc gtc caa gtc aac gga tgg   1843
Gly Lys Val Gly Thr Leu Met Thr Gly Ser Val Gln Val Asn Gly Trp
                570                 575                 580

gac aac gaa aac acc aca att ttc gac ggc gac ctc tct cag ttc ctc   1891
Asp Asn Glu Asn Thr Thr Ile Phe Asp Gly Asp Leu Ser Gln Phe Leu
            585                 590                 595

gac ctc gca gtc cgc tcc ggc gac gcc ttc gac gac gaa acc ccc ggc   1939
Asp Leu Ala Val Arg Ser Gly Asp Ala Phe Asp Asp Glu Thr Pro Gly
        600                 605                 610

gtc atg atc tcc acc acc tac gcc gac caa tcc gac ctc gaa gta ggc   1987
Val Met Ile Ser Thr Thr Tyr Ala Asp Gln Ser Asp Leu Glu Val Gly
    615                 620                 625

gac acc gtc acc gtc aac ccc tac gga tcc gac gac ggc atc cgc gtc   2035
Asp Thr Val Thr Val Asn Pro Tyr Gly Ser Asp Asp Gly Ile Arg Val
630                 635                 640                 645

ccc atc acc ggc atc tac gca gaa acc aac ctc gtc gga cac ctc atg   2083
Pro Ile Thr Gly Ile Tyr Ala Glu Thr Asn Leu Val Gly His Leu Met
                650                 655                 660

gtc aac gca gcc gcc acc aac cga gtc ctc acc tcc gcg gac acc tac   2131
Val Asn Ala Ala Ala Thr Asn Arg Val Leu Thr Ser Ala Asp Thr Tyr
            665                 670                 675

cac cgg tcc caa atc ttc gtc aac ggc gac ggc tcc acc acc aac gaa   2179
His Arg Ser Gln Ile Phe Val Asn Gly Asp Gly Ser Thr Thr Asn Glu
        680                 685                 690

gaa ctc cgc gac atc ctc gtc gac gcc gta gcc ccc ttc ctc atc gtc   2227
Glu Leu Arg Asp Ile Leu Val Asp Ala Val Ala Pro Phe Leu Ile Val
    695                 700                 705

caa gtg aaa tcc aaa gat gaa ttc cgc gga agc ctc ggc acc caa atc   2275
Gln Val Lys Ser Lys Asp Glu Phe Arg Gly Ser Leu Gly Thr Gln Ile
710                 715                 720                 725

aac caa ttg ctc ggc atc atc tac gga ctg ctc gcc ctg gca gtg atc   2323
Asn Gln Leu Leu Gly Ile Ile Tyr Gly Leu Leu Ala Leu Ala Val Ile
                730                 735                 740

atc gca gtc ctg gga atc gtc aac aca ctg ttc ctc tcc atc agc gaa   2371
Ile Ala Val Leu Gly Ile Val Asn Thr Leu Phe Leu Ser Ile Ser Glu
            745                 750                 755

cgc acc cgc gaa atc gga atc ctc cgc gcc acc ggc gtc caa cga gga   2419
```

```
Arg Thr Arg Glu Ile Gly Ile Leu Arg Ala Thr Gly Val Gln Arg Gly
        760                 765                 770

caa atc cgc cgc atg att acc ctc gaa tcc gtc atc ctc tcc atc cac   2467
Gln Ile Arg Arg Met Ile Thr Leu Glu Ser Val Ile Leu Ser Ile His
    775                 780                 785

ggc gca atc cac gga ctc ctc cta ggt aca ttt atc ggc tgg gca atc   2515
Gly Ala Ile His Gly Leu Leu Leu Gly Thr Phe Ile Gly Trp Ala Ile
790                 795                 800                 805

gtc agt tgt ctc cgc acc cga ggc atg gca ccc gtc gaa ttc ccc tgg   2563
Val Ser Cys Leu Arg Thr Arg Gly Met Ala Pro Val Glu Phe Pro Trp
                810                 815                 820

acc caa atc gga tta atg ctc atc tcc gca atc atc atc gga ggc ata   2611
Thr Gln Ile Gly Leu Met Leu Ile Ser Ala Ile Ile Ile Gly Gly Ile
            825                 830                 835

gca gcc ctc atc cca gcc aac cga gcc tcc cga atc tcc cct ttg gaa   2659
Ala Ala Leu Ile Pro Ala Asn Arg Ala Ser Arg Ile Ser Pro Leu Glu
        840                 845                 850

gca atc aac taacagtctg catcggcaac ctc                            2691
Ala Ile Asn
    855


<210> 2760
<211> 856
<212> PRT
<213> Corynebacterium glutamicum

<400> 2760
Met Ala Leu Thr Val Leu Ser Val Val Leu Gly Thr Ala Phe Leu Cys
  1               5                  10                  15

Gly Ser Leu Leu Leu Thr His Ser Leu Glu Arg Thr Phe Ser Ser Ile
             20                  25                  30

Val Asp Ala Gly Val Glu Gly Val Asp Val Gly Val Ile Ala Gln Gln
         35                  40                  45

Asn Asn Pro Asp Gly Val Pro Phe Ser Val Ile Ala Glu Ile Glu Gln
     50                  55                  60

Tyr Pro Glu Val Arg Ala Val Asn Ile Ile Gly Asp Gly Pro Gly Met
 65                  70                  75                  80

Pro Ser Gly Thr Thr Met Thr Gly Gln Ser Ala Leu Ile Leu Thr Asp
                 85                  90                  95

Ser Asp Gly Asn Pro Leu Gln Ala Gly Ser Ser Gly Thr His Pro Leu
            100                 105                 110

Ala Ile Tyr Pro Gln Gly Glu Trp Val Ser Pro Glu Pro Thr Leu Ile
        115                 120                 125

Asp Gly His Phe Pro Thr Lys Pro Asp Glu Val Val Val Asn Ala Ser
    130                 135                 140
```

```
Ala Ala Lys Arg Gly Gly Leu Ser Leu Gly Asp His Leu Thr Ile Val
145                 150                 155                 160

Thr Pro Thr Glu Arg Ile Asp Ala Thr Leu Ser Gly Thr Phe Glu Ser
                165                 170                 175

Asn Thr Asp Val Ala Gly Trp Val Gly Val Gly Phe Thr Pro Gln Arg
            180                 185                 190

Tyr Val Glu Leu Leu Thr Asn Gly Thr Asp Ala Ser Gln Ile Thr Ile
        195                 200                 205

Ala Val Asn Asp Gly Ala Asp Pro Met Ala Val Arg Asn Arg Ile Gly
    210                 215                 220

Lys Asn His Arg Asp Leu Leu Pro Leu Leu Pro Glu Gln Ile Ile Asp
225                 230                 235                 240

Gln Thr Thr Gly Asp Thr Asp Arg Gln Leu Glu Phe Met Thr Tyr Val
                245                 250                 255

Leu Leu Ala Phe Ala Ala Ile Ala Leu Ile Val Gly Ser Phe Ile Ile
            260                 265                 270

Ala Asn Thr Phe Ala Met Ile Val Ala Gln Arg Thr Gly Glu Phe Ala
        275                 280                 285

Leu Leu Arg Ser Ile Gly Val Ser Thr Phe Gln Ile Gly Phe Ser Val
    290                 295                 300

Ile Met Glu Ala Val Phe Val Gly Leu Ile Gly Gly Phe Ile Gly Ile
305                 310                 315                 320

Ala Val Gly Phe Gly Val Val Asn Ala Leu Val Gln Val Leu Asn Gln
                325                 330                 335

Phe Gly Asp Thr Leu Ser Ser Ile Asp Ile Thr Tyr Asn Ala Gly Ser
            340                 345                 350

Phe Ile Phe Pro Val Leu Phe Ala Val Thr Ala Thr Val Leu Ser Ser
        355                 360                 365

Ile Ser Pro Ala His Arg Ala Gly Asn Leu Pro Pro Val Gln Ala Phe
    370                 375                 380

Glu Ser Ser Asp Ala Arg Ser Asp Ala Leu Gly Arg Ile Arg Phe Leu
385                 390                 395                 400

Val Ala Ala Val Met Leu Thr Leu Gly Ile Ser Leu Thr Ile Ala Gly
                405                 410                 415

Ala Val Val Ser Ala Ile Asn Gly Asp Glu Phe Lys Thr Glu Thr Arg
            420                 425                 430

Leu Ala Phe Ile Gly Ala Gly Leu Leu Leu Val Phe Phe Ser Leu Ser
        435                 440                 445

Leu Ser Gly Pro Ala Leu Met Val Ala Thr Ser Gln Thr Leu Gly Val
    450                 455                 460

Ala Ile Met Ser Pro Phe Arg Ala Val Gly Lys Leu Ala Gln Arg Asn
```

```
465                 470                 475                 480

Thr Leu Arg Asn Pro Arg Arg Ser Ala Thr Thr Ala Leu Ala Val Thr
                485                 490                 495

Leu Ser Val Gly Leu Val Ala Cys Val Gly Val Ile Gly Ala Thr Thr
            500                 505                 510

Arg Ala Ser Val Phe Gly Ser Met Glu Ser Thr Ile Lys Ser Pro Tyr
        515                 520                 525

Val Leu Asp Ser Ile Gly Gly Thr Met Ile Pro Gly Gln Pro Ala Gly
    530                 535                 540

Gly Ser Arg Ser Leu Ser Met Ser Ala Ala Val Ala Gln Glu Ile Ala
545                 550                 555                 560

Gln Thr Arg Gly Val Gly Lys Val Gly Thr Leu Met Thr Gly Ser Val
                565                 570                 575

Gln Val Asn Gly Trp Asp Asn Glu Asn Thr Thr Ile Phe Asp Gly Asp
            580                 585                 590

Leu Ser Gln Phe Leu Asp Leu Ala Val Arg Ser Gly Asp Ala Phe Asp
        595                 600                 605

Asp Glu Thr Pro Gly Val Met Ile Ser Thr Thr Tyr Ala Asp Gln Ser
    610                 615                 620

Asp Leu Glu Val Gly Asp Thr Val Thr Val Asn Pro Tyr Gly Ser Asp
625                 630                 635                 640

Asp Gly Ile Arg Val Pro Ile Thr Gly Ile Tyr Ala Glu Thr Asn Leu
                645                 650                 655

Val Gly His Leu Met Val Asn Ala Ala Ala Thr Asn Arg Val Leu Thr
            660                 665                 670

Ser Ala Asp Thr Tyr His Arg Ser Gln Ile Phe Val Asn Gly Asp Gly
        675                 680                 685

Ser Thr Thr Asn Glu Glu Leu Arg Asp Ile Leu Val Asp Ala Val Ala
    690                 695                 700

Pro Phe Leu Ile Val Gln Val Lys Ser Lys Asp Glu Phe Arg Gly Ser
705                 710                 715                 720

Leu Gly Thr Gln Ile Asn Gln Leu Leu Gly Ile Ile Tyr Gly Leu Leu
                725                 730                 735

Ala Leu Ala Val Ile Ile Ala Val Leu Gly Ile Val Asn Thr Leu Phe
            740                 745                 750

Leu Ser Ile Ser Glu Arg Thr Arg Glu Ile Gly Ile Leu Arg Ala Thr
        755                 760                 765

Gly Val Gln Arg Gly Gln Ile Arg Arg Met Ile Thr Leu Glu Ser Val
    770                 775                 780

Ile Leu Ser Ile His Gly Ala Ile His Gly Leu Leu Leu Gly Thr Phe
785                 790                 795                 800
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Ile Gly Trp Ala Ile Val Ser Cys Leu Arg Thr Arg Gly Met Ala Pro
               805                 810                 815

Val Glu Phe Pro Trp Thr Gln Ile Gly Leu Met Leu Ile Ser Ala Ile
            820                 825                 830

Ile Ile Gly Gly Ile Ala Ala Leu Ile Pro Ala Asn Arg Ala Ser Arg
        835                 840                 845

Ile Ser Pro Leu Glu Ala Ile Asn
    850                 855


<210> 2761
<211> 930
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(907)
<223> RXA02496

<400> 2761
cgggacgcgc gtctactgca actaggtgga cagtattgct gcccacatct aatacaccta 60

atctcacacc taaaggttag acggtctagg gtggcaaagt gtg aat cgg tca aat   115
                                            Val Asn Arg Ser Asn
                                              1               5

tct tct tcg gta ttt tta ggt ttc ccc gag tct tcg cca gcg gcg gca   163
Ser Ser Ser Val Phe Leu Gly Phe Pro Glu Ser Ser Pro Ala Ala Ala
                10                  15                  20

tcg att cgt gct ggg gag gaa ctc cct ctt gat ttc cca cgt gaa tgg   211
Ser Ile Arg Ala Gly Glu Glu Leu Pro Leu Asp Phe Pro Arg Glu Trp
             25                  30                  35

tat gaa ttc acg gat cca act gat att gag cat gta ttt agc atc gat   259
Tyr Glu Phe Thr Asp Pro Thr Asp Ile Glu His Val Phe Ser Ile Asp
         40                  45                  50

tta acg tgg ctt gag tct aat tgg aat tgc acc ttt ggt acc ccc gat   307
Leu Thr Trp Leu Glu Ser Asn Trp Asn Cys Thr Phe Gly Thr Pro Asp
     55                  60                  65

tgt tta ggt att gat tcc gaa aac gcc gac gtg ggt tgt tgc ggc cac   355
Cys Leu Gly Ile Asp Ser Glu Asn Ala Asp Val Gly Cys Cys Gly His
 70                  75                  80                  85

ggt gca ttc tta gca gat gag aca gat cga gat cag ctt tat gat gcc   403
Gly Ala Phe Leu Ala Asp Glu Thr Asp Arg Asp Gln Leu Tyr Asp Ala
                90                  95                 100

gtt gct cag atg ccc gct aag tat tgg cag cta cgc ccc gcc tcc acg   451
Val Ala Gln Met Pro Ala Lys Tyr Trp Gln Leu Arg Pro Ala Ser Thr
            105                 110                 115

gac tcg ttt tta gca tcc gat gac ggc acc gac att gag ccg tgg ctg   499
Asp Ser Phe Leu Ala Ser Asp Asp Gly Thr Asp Ile Glu Pro Trp Leu
```

```
        120                 125                 130

aca tgg gat gaa tta gat gat gaa gac ggc aat ccc gag ccc gct ttg   547
Thr Trp Asp Glu Leu Asp Asp Glu Asp Gly Asn Pro Glu Pro Ala Leu
    135                 140                 145

aag aca act gtg gtc aac ggc gcc tgt att ttt gcc aac agg gcg ggt   595
Lys Thr Thr Val Val Asn Gly Ala Cys Ile Phe Ala Asn Arg Ala Gly
150                 155                 160                 165

tgg gaa aca ggc gcg ggg tgt gcg ctg cat cag tgg ggc gtg aac gca   643
Trp Glu Thr Gly Ala Gly Cys Ala Leu His Gln Trp Gly Val Asn Ala
                170                 175                 180

aat gag gat cta acc gtc gtc aag cct gaa gtt tgt tgg cag ctc ccg   691
Asn Glu Asp Leu Thr Val Val Lys Pro Glu Val Cys Trp Gln Leu Pro
            185                 190                 195

ctg cgc cgc ctg gag gcc tgg gaa gag cgc ccc gac ggg caa gaa atc   739
Leu Arg Arg Leu Glu Ala Trp Glu Glu Arg Pro Asp Gly Gln Glu Ile
        200                 205                 210

ttg cgc acc aca att act gaa tac aac cgg cgc ggc tgg ggc aac ggc   787
Leu Arg Thr Thr Ile Thr Glu Tyr Asn Arg Arg Gly Trp Gly Asn Gly
    215                 220                 225

ggc gag gat ttc gac tgg tac tgc acc acc tct ccg cgc tgc cac acc   835
Gly Glu Asp Phe Asp Trp Tyr Cys Thr Thr Ser Pro Arg Cys His Thr
230                 235                 240                 245

aat gcc gaa ccc atg tgg aaa aca cag gaa aca gaa ctc cgt gca ctc   883
Asn Ala Glu Pro Met Trp Lys Thr Gln Glu Thr Glu Leu Arg Ala Leu
                250                 255                 260

atg gga cca aac tcc tac gag gtg tgacgtaaat atttggaagc acg         930
Met Gly Pro Asn Ser Tyr Glu Val
            265
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<210> 2762
<211> 269
<212> PRT
<213> Corynebacterium glutamicum

<400> 2762

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Val Asn Arg Ser Asn Ser Ser Ser Val Phe Leu Gly Phe Pro Glu Ser
  1               5                  10                  15

Ser Pro Ala Ala Ala Ser Ile Arg Ala Gly Glu Glu Leu Pro Leu Asp
             20                  25                  30

Phe Pro Arg Glu Trp Tyr Glu Phe Thr Asp Pro Thr Asp Ile Glu His
         35                  40                  45

Val Phe Ser Ile Asp Leu Thr Trp Leu Glu Ser Asn Trp Asn Cys Thr
     50                  55                  60

Phe Gly Thr Pro Asp Cys Leu Gly Ile Asp Ser Glu Asn Ala Asp Val
 65                  70                  75                  80

Gly Cys Cys Gly His Gly Ala Phe Leu Ala Asp Glu Thr Asp Arg Asp
```

```
                85                  90                  95

Gln Leu Tyr Asp Ala Val Ala Gln Met Pro Ala Lys Tyr Trp Gln Leu
            100                 105                 110

Arg Pro Ala Ser Thr Asp Ser Phe Leu Ala Ser Asp Asp Gly Thr Asp
        115                 120                 125

Ile Glu Pro Trp Leu Thr Trp Asp Glu Leu Asp Asp Glu Asp Gly Asn
    130                 135                 140

Pro Glu Pro Ala Leu Lys Thr Thr Val Val Asn Gly Ala Cys Ile Phe
145                 150                 155                 160

Ala Asn Arg Ala Gly Trp Glu Thr Gly Ala Gly Cys Ala Leu His Gln
                165                 170                 175

Trp Gly Val Asn Ala Asn Glu Asp Leu Thr Val Val Lys Pro Glu Val
            180                 185                 190

Cys Trp Gln Leu Pro Leu Arg Arg Leu Glu Ala Trp Glu Glu Arg Pro
        195                 200                 205

Asp Gly Gln Glu Ile Leu Arg Thr Thr Ile Thr Glu Tyr Asn Arg Arg
    210                 215                 220

Gly Trp Gly Asn Gly Gly Glu Asp Phe Asp Trp Tyr Cys Thr Thr Ser
225                 230                 235                 240

Pro Arg Cys His Thr Asn Ala Glu Pro Met Trp Lys Thr Gln Glu Thr
                245                 250                 255

Glu Leu Arg Ala Leu Met Gly Pro Asn Ser Tyr Glu Val
            260                 265


<210> 2763
<211> 927
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(904)
<223> RXA02498

<400> 2763
caaggtagaa atttgtccgt gggcacttcg tgaaggtgtg atcctcacca ggatcgacaa 60

aggactcgag taacatttac ccggaaagga gttggcgaaa atg agt gaa gag aaa   115
                                            Met Ser Glu Glu Lys
                                              1               5

ctc aca gtc gct gag ctg atg gcg cgt gcc gcg aaa gag gga cgc tcc   163
Leu Thr Val Ala Glu Leu Met Ala Arg Ala Ala Lys Glu Gly Arg Ser
                10                  15                  20

acc gat gct ccc cga cga cgc agg cgc cgc agc atc gaa gac ggt ggc   211
Thr Asp Ala Pro Arg Arg Arg Arg Arg Arg Ser Ile Glu Asp Gly Gly
            25                  30                  35
```

```
gta tcc gtt gct gag ctg acc ggc tcc att cct gcc gtt aag gaa aag   259
Val Ser Val Ala Glu Leu Thr Gly Ser Ile Pro Ala Val Lys Glu Lys
         40                  45                  50

ccc gcg gag tcc aag cac tcc agc gtg ccc atc gat gca cca gca gaa   307
Pro Ala Glu Ser Lys His Ser Ser Val Pro Ile Asp Ala Pro Ala Glu
     55                  60                  65

cct gag gtt gtt gag gcc ccc aag cct gag ccc gcc gaa gaa gta gaa   355
Pro Glu Val Val Glu Ala Pro Lys Pro Glu Pro Ala Glu Glu Val Glu
 70                  75                  80                  85

gtg gct tcg gtg gag ggc gac gtc gat aag cag gaa acc cct gag cgt   403
Val Ala Ser Val Glu Gly Asp Val Asp Lys Gln Glu Thr Pro Glu Arg
                 90                  95                 100

ccg gcg ccg agc aac gaa gaa acc atg gtg ctg cgc atc gtg gat gaa   451
Pro Ala Pro Ser Asn Glu Glu Thr Met Val Leu Arg Ile Val Asp Glu
            105                 110                 115

aaa gat cca att agc ttg acg acg ggc gcg ttc ccc gtg gtt ccg gca   499
Lys Asp Pro Ile Ser Leu Thr Thr Gly Ala Phe Pro Val Val Pro Ala
        120                 125                 130

gtt gcc gcc aag ccg gcg ccc gta gtg cgc gcg gag aag gac gcc gat   547
Val Ala Ala Lys Pro Ala Pro Val Val Arg Ala Glu Lys Asp Ala Asp
    135                 140                 145

gtg gag act gcc gta aag gca gat ttc gca gag gtg gaa gtc gat aac   595
Val Glu Thr Ala Val Lys Ala Asp Phe Ala Glu Val Glu Val Asp Asn
150                 155                 160                 165

act gac acc acg cag atg gct gtg gtg gaa gaa gtt gac gag gag cca   643
Thr Asp Thr Thr Gln Met Ala Val Val Glu Glu Val Asp Glu Glu Pro
                170                 175                 180

gag caa gaa aac aaa atg tcc gta ttc gcg atc atc atg atg gcg atc   691
Glu Gln Glu Asn Lys Met Ser Val Phe Ala Ile Ile Met Met Ala Ile
            185                 190                 195

gtc gga gtt gtt ctc ggt gtc gtt gta ttc ctc ggc ttt gaa atg ctg   739
Val Gly Val Val Leu Gly Val Val Val Phe Leu Gly Phe Glu Met Leu
        200                 205                 210

tgg gag cgc ctg aac aag tgg atc gtc gct gtt ctg gca gtc ggc gtg   787
Trp Glu Arg Leu Asn Lys Trp Ile Val Ala Val Leu Ala Val Gly Val
    215                 220                 225

acc ttg gga atg gtg ggc atc atc cac gct ttg cgc acc tca cgt gat   835
Thr Leu Gly Met Val Gly Ile Ile His Ala Leu Arg Thr Ser Arg Asp
230                 235                 240                 245

ggt ttc agc atg gtt ctc gca gga atc gtg ggc ctg gtc atg acg ttc   883
Gly Phe Ser Met Val Leu Ala Gly Ile Val Gly Leu Val Met Thr Phe
                250                 255                 260

ggg ccg ctg gca atc gtc atg taatttgtcg ttttgggccc ccg             927
Gly Pro Leu Ala Ile Val Met
            265
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<210> 2764
<211> 268
<212> PRT
<213> Corynebacterium glutamicum

<400> 2764
Met Ser Glu Glu Lys Leu Thr Val Ala Glu Leu Met Ala Arg Ala Ala
1 5 10 15

Lys Glu Gly Arg Ser Thr Asp Ala Pro Arg Arg Arg Arg Arg Arg Ser
20 25 30

Ile Glu Asp Gly Gly Val Ser Val Ala Glu Leu Thr Gly Ser Ile Pro
35 40 45

Ala Val Lys Glu Lys Pro Ala Glu Ser Lys His Ser Ser Val Pro Ile
50 55 60

Asp Ala Pro Ala Glu Pro Glu Val Val Glu Ala Pro Lys Pro Glu Pro
65 70 75 80

Ala Glu Glu Val Glu Val Ala Ser Val Glu Gly Asp Val Asp Lys Gln
85 90 95

Glu Thr Pro Glu Arg Pro Ala Pro Ser Asn Glu Glu Thr Met Val Leu
100 105 110

Arg Ile Val Asp Glu Lys Asp Pro Ile Ser Leu Thr Thr Gly Ala Phe
115 120 125

Pro Val Val Pro Ala Val Ala Ala Lys Pro Ala Pro Val Val Arg Ala
130 135 140

Glu Lys Asp Ala Asp Val Glu Thr Ala Val Lys Ala Asp Phe Ala Glu
145 150 155 160

Val Glu Val Asp Asn Thr Asp Thr Thr Gln Met Ala Val Val Glu Glu
165 170 175

Val Asp Glu Glu Pro Glu Gln Glu Asn Lys Met Ser Val Phe Ala Ile
180 185 190

Ile Met Met Ala Ile Val Gly Val Val Leu Gly Val Val Val Phe Leu
195 200 205

Gly Phe Glu Met Leu Trp Glu Arg Leu Asn Lys Trp Ile Val Ala Val
210 215 220

Leu Ala Val Gly Val Thr Leu Gly Met Val Gly Ile Ile His Ala Leu
225 230 235 240

Arg Thr Ser Arg Asp Gly Phe Ser Met Val Leu Ala Gly Ile Val Gly
245 250 255

Leu Val Met Thr Phe Gly Pro Leu Ala Ile Val Met
260 265

<210> 2765
<211> 222
<212> DNA

<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(199)
<223> RXA02500

<400> 2765
acgcgggtta gatttttgct cgcgatccga aagtgcactt cggcaaaaag tgctggcagg 60

ttttgtacgt acaacatcga tttaagcgag ggaaaccgta atg ggt tct gtc atc 115
Met Gly Ser Val Ile
1 5

aag aag cgc cgc aag cgc atg tcc aag aag aag cac cgc aag atg ctg 163
Lys Lys Arg Arg Lys Arg Met Ser Lys Lys Lys His Arg Lys Met Leu
10 15 20

cgc cgt act cgt gtc cag cgt aga aaa ttg ggc aag taagccttca 209
Arg Arg Thr Arg Val Gln Arg Arg Lys Leu Gly Lys
25 30

attgagcttc aaa 222

<210> 2766
<211> 33
<212> PRT
<213> Corynebacterium glutamicum

<400> 2766
Met Gly Ser Val Ile Lys Lys Arg Arg Lys Arg Met Ser Lys Lys Lys
1 5 10 15

His Arg Lys Met Leu Arg Arg Thr Arg Val Gln Arg Arg Lys Leu Gly
20 25 30

Lys

<210> 2767
<211> 1005
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(982)
<223> RXA02506

<400> 2767
cctttccctg aactctaagc aattgtgatc tatagtacaa atgcataaac attaaccgtg 60

atatccatct cttgcatacc ggccgaaagg tttagcacac atg cac ctc aat cag 115
Met His Leu Asn Gln
1 5

ctc gaa ttt ttc atc gca gta gcc caa cac gga cag atc aac cgc gcc 163
Leu Glu Phe Phe Ile Ala Val Ala Gln His Gly Gln Ile Asn Arg Ala
10 15 20

```
gcc gaa gaa ctc ctc att tcc caa ccc gct ctc agc cga cag atc tcc   211
Ala Glu Glu Leu Leu Ile Ser Gln Pro Ala Leu Ser Arg Gln Ile Ser
             25                  30                  35

gca ctt gaa aaa tcc gtc gga gct cca ctc ttc gaa cgc cat tcc cgc   259
Ala Leu Glu Lys Ser Val Gly Ala Pro Leu Phe Glu Arg His Ser Arg
         40                  45                  50

ggt gtc tcc ctc aca aag gcc gga gaa atc ctc cac gaa gaa gcc ctc   307
Gly Val Ser Leu Thr Lys Ala Gly Glu Ile Leu His Glu Glu Ala Leu
     55                  60                  65

cga acg ctt agc agg atg caa tcg gta gtc gat gaa atc caa tcc ggt   355
Arg Thr Leu Ser Arg Met Gln Ser Val Val Asp Glu Ile Gln Ser Gly
 70                  75                  80                  85

gag cac ctc atc acc agc atc aac atc gga gtt ccc cct gga atc ccc   403
Glu His Leu Ile Thr Ser Ile Asn Ile Gly Val Pro Pro Gly Ile Pro
                 90                  95                 100

atc gac tgg ttg cgc tgc caa ctc atc gat tta ggc ccc gag acc cgc   451
Ile Asp Trp Leu Arg Cys Gln Leu Ile Asp Leu Gly Pro Glu Thr Arg
            105                 110                 115

att tca ctg atc gaa tcc ccc acc gat gat cag cta aaa ctt ctt aaa   499
Ile Ser Leu Ile Glu Ser Pro Thr Asp Asp Gln Leu Lys Leu Leu Lys
        120                 125                 130

caa cgc gaa ctc gac atc gcc ctt tgt cga cgc caa agc gag gcc ttt   547
Gln Arg Glu Leu Asp Ile Ala Leu Cys Arg Arg Gln Ser Glu Ala Phe
    135                 140                 145

gcc acc aca ctt gtc cac gaa caa gaa ctg gga atc gtc gtc cga aaa   595
Ala Thr Thr Leu Val His Glu Gln Glu Leu Gly Ile Val Val Arg Lys
150                 155                 160                 165

aac tcc gaa ctg cac caa aaa gtc gca gga aaa gac aac gcc aca ctc   643
Asn Ser Glu Leu His Gln Lys Val Ala Gly Lys Asp Asn Ala Thr Leu
                170                 175                 180

ttc gat ctt gaa ggg ctt cga gtc ctc gca cac tcc cgc ggt gaa gta   691
Phe Asp Leu Glu Gly Leu Arg Val Leu Ala His Ser Arg Gly Glu Val
            185                 190                 195

aga att cag gaa gaa atc ctc aaa aac gcc atg ctc gcc gca gga gtt   739
Arg Ile Gln Glu Glu Ile Leu Lys Asn Ala Met Leu Ala Ala Gly Val
        200                 205                 210

aat gcc acg tgg atc ttc cga aaa ttt ggg caa tat agc tca ctg atc   787
Asn Ala Thr Trp Ile Phe Arg Lys Phe Gly Gln Tyr Ser Ser Leu Ile
    215                 220                 225

gca gac ctt gtc cag gcc gat gtc gca ctc aca aca gag gaa tcc gcc   835
Ala Asp Leu Val Gln Ala Asp Val Ala Leu Thr Thr Glu Glu Ser Ala
230                 235                 240                 245

cgc acc aac ttc ccc agc tgg caa tgg gtc ccc atc gaa ggc gaa gac   883
Arg Thr Asn Phe Pro Ser Trp Gln Trp Val Pro Ile Glu Gly Glu Asp
                250                 255                 260
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```
gcc tcc gga aat gac ctt gtt gtt cgc acc tgg atc acc tgg aac ccc   931
Ala Ser Gly Asn Asp Leu Val Val Arg Thr Trp Ile Thr Trp Asn Pro
            265                 270                 275

caa ccc acc ccc gcg gtg aag gcc ctg atc cag aaa ttt att gac gga   979
Gln Pro Thr Pro Ala Val Lys Ala Leu Ile Gln Lys Phe Ile Asp Gly
        280                 285                 290

aac tgagttctaa acagccgcca tga                                    1005
Asn
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<210> 2768
<211> 294
<212> PRT
<213> Corynebacterium glutamicum

<400> 2768

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Met His Leu Asn Gln Leu Glu Phe Phe Ile Ala Val Ala Gln His Gly
  1               5                  10                  15

Gln Ile Asn Arg Ala Ala Glu Glu Leu Leu Ile Ser Gln Pro Ala Leu
             20                  25                  30

Ser Arg Gln Ile Ser Ala Leu Glu Lys Ser Val Gly Ala Pro Leu Phe
         35                  40                  45

Glu Arg His Ser Arg Gly Val Ser Leu Thr Lys Ala Gly Glu Ile Leu
     50                  55                  60

His Glu Glu Ala Leu Arg Thr Leu Ser Arg Met Gln Ser Val Val Asp
 65                  70                  75                  80

Glu Ile Gln Ser Gly Glu His Leu Ile Thr Ser Ile Asn Ile Gly Val
                 85                  90                  95

Pro Pro Gly Ile Pro Ile Asp Trp Leu Arg Cys Gln Leu Ile Asp Leu
            100                 105                 110

Gly Pro Glu Thr Arg Ile Ser Leu Ile Glu Ser Pro Thr Asp Asp Gln
        115                 120                 125

Leu Lys Leu Leu Lys Gln Arg Glu Leu Asp Ile Ala Leu Cys Arg Arg
    130                 135                 140

Gln Ser Glu Ala Phe Ala Thr Thr Leu Val His Glu Gln Glu Leu Gly
145                 150                 155                 160

Ile Val Val Arg Lys Asn Ser Glu Leu His Gln Lys Val Ala Gly Lys
                165                 170                 175

Asp Asn Ala Thr Leu Phe Asp Leu Glu Gly Leu Arg Val Leu Ala His
            180                 185                 190

Ser Arg Gly Glu Val Arg Ile Gln Glu Glu Ile Leu Lys Asn Ala Met
        195                 200                 205

Leu Ala Ala Gly Val Asn Ala Thr Trp Ile Phe Arg Lys Phe Gly Gln
    210                 215                 220
```

```
Tyr Ser Ser Leu Ile Ala Asp Leu Val Gln Ala Asp Val Ala Leu Thr
225                 230                 235                 240

Thr Glu Glu Ser Ala Arg Thr Asn Phe Pro Ser Trp Gln Trp Val Pro
                245                 250                 255

Ile Glu Gly Glu Asp Ala Ser Gly Asn Asp Leu Val Val Arg Thr Trp
            260                 265                 270

Ile Thr Trp Asn Pro Gln Pro Thr Pro Ala Val Lys Ala Leu Ile Gln
        275                 280                 285

Lys Phe Ile Asp Gly Asn
    290
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<210> 2769
<211> 860
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(837)
<223> RXA02514

<400> 2769

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aac tcc cac aac cca acc cca gta acc atc acg gtt act ggc aag ggt   48
Asn Ser His Asn Pro Thr Pro Val Thr Ile Thr Val Thr Gly Lys Gly
  1               5                  10                  15

gaa ggc gtt acc tct ttc ggc gca atc tcc atc gag gtt gaa gcg ggc   96
Glu Gly Val Thr Ser Phe Gly Ala Ile Ser Ile Glu Val Glu Ala Gly
             20                  25                  30

gca gac gct atc gtc gca ctg cag tac gtc gga tcc ggc acc cac gct   144
Ala Asp Ala Ile Val Ala Leu Gln Tyr Val Gly Ser Gly Thr His Ala
         35                  40                  45

gac aac gtc gaa ttc atc gtt ggc gac aac gca cgc ctg acc gtc atc   192
Asp Asn Val Glu Phe Ile Val Gly Asp Asn Ala Arg Leu Thr Val Ile
     50                  55                  60

acg gac acc cac tgg aac gct gac gca gtt cac ctg agc aac cag ctt   240
Thr Asp Thr His Trp Asn Ala Asp Ala Val His Leu Ser Asn Gln Leu
 65                  70                  75                  80

gca cag ctg gga cgc gac gca act cta cgc cac acc gtg gca acc ttc   288
Ala Gln Leu Gly Arg Asp Ala Thr Leu Arg His Thr Val Ala Thr Phe
                 85                  90                  95

ggt gga gaa gta gtc cgc atc gtc cca cgc gtg cgt ttc acc gca cca   336
Gly Gly Glu Val Val Arg Ile Val Pro Arg Val Arg Phe Thr Ala Pro
            100                 105                 110

ggt ggc gac gca gaa atg ctc ggc gtc tac ttc gca gat gat gga cag   384
Gly Gly Asp Ala Glu Met Leu Gly Val Tyr Phe Ala Asp Asp Gly Gln
        115                 120                 125

tac ttc gag cag cgc ctg ctg gtt gac cac gct gta cca aac tgt cgc   432
Tyr Phe Glu Gln Arg Leu Leu Val Asp His Ala Val Pro Asn Cys Arg
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```
    130                 135                 140

tcc aac gtc ttg tac aag ggc gca ctt cag ggt gac aag aac tct gac   480
Ser Asn Val Leu Tyr Lys Gly Ala Leu Gln Gly Asp Lys Asn Ser Asp
145                 150                 155                 160

aag cca gat gcc cgt acc tgc tgg gtt ggc gat gtg ctc atc cgc tca   528
Lys Pro Asp Ala Arg Thr Cys Trp Val Gly Asp Val Leu Ile Arg Ser
                165                 170                 175

aac gcc cac ggc act gac acc tac gaa gct aac cgc tca ctc gtc ctc   576
Asn Ala His Gly Thr Asp Thr Tyr Glu Ala Asn Arg Ser Leu Val Leu
            180                 185                 190

acc gag ggt gca cgc gca gac gct att cca aac ctc gag att gaa acc   624
Thr Glu Gly Ala Arg Ala Asp Ala Ile Pro Asn Leu Glu Ile Glu Thr
        195                 200                 205

ggc cag atc gtt ggc gca gga cac gca gca acc gtc ggt cgt ttc gac   672
Gly Gln Ile Val Gly Ala Gly His Ala Ala Thr Val Gly Arg Phe Asp
    210                 215                 220

gac gag cac gtg ttc tac ctc cag gcc cgt ggt att cct gca gag gaa   720
Asp Glu His Val Phe Tyr Leu Gln Ala Arg Gly Ile Pro Ala Glu Glu
225                 230                 235                 240

gca cgc cgc ctc atc gtc cgc ggt ttc ttc aac gaa gtg atc aac aag   768
Ala Arg Arg Leu Ile Val Arg Gly Phe Phe Asn Glu Val Ile Asn Lys
                245                 250                 255

gtc cca gtt gaa tcc atc cgc ggg gaa ttg gac aac cga gtc agc tcg   816
Val Pro Val Glu Ser Ile Arg Gly Glu Leu Asp Asn Arg Val Ser Ser
            260                 265                 270

gaa ctc gca gtt ctt ggc atg taattaagcc aaagtaacta agc             860
Glu Leu Ala Val Leu Gly Met
        275
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<210> 2770
<211> 279
<212> PRT
<213> Corynebacterium glutamicum

<400> 2770

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Asn Ser His Asn Pro Thr Pro Val Thr Ile Thr Val Thr Gly Lys Gly
  1               5                  10                  15

Glu Gly Val Thr Ser Phe Gly Ala Ile Ser Ile Glu Val Glu Ala Gly
             20                  25                  30

Ala Asp Ala Ile Val Ala Leu Gln Tyr Val Gly Ser Gly Thr His Ala
         35                  40                  45

Asp Asn Val Glu Phe Ile Val Gly Asp Asn Ala Arg Leu Thr Val Ile
     50                  55                  60

Thr Asp Thr His Trp Asn Ala Asp Ala Val His Leu Ser Asn Gln Leu
 65                  70                  75                  80

Ala Gln Leu Gly Arg Asp Ala Thr Leu Arg His Thr Val Ala Thr Phe
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```
                85                  90                  95

Gly Gly Glu Val Val Arg Ile Val Pro Arg Val Arg Phe Thr Ala Pro
            100                 105                 110

Gly Gly Asp Ala Glu Met Leu Gly Val Tyr Phe Ala Asp Asp Gly Gln
        115                 120                 125

Tyr Phe Glu Gln Arg Leu Leu Val Asp His Ala Val Pro Asn Cys Arg
    130                 135                 140

Ser Asn Val Leu Tyr Lys Gly Ala Leu Gln Gly Asp Lys Asn Ser Asp
145                 150                 155                 160

Lys Pro Asp Ala Arg Thr Cys Trp Val Gly Asp Val Leu Ile Arg Ser
                165                 170                 175

Asn Ala His Gly Thr Asp Thr Tyr Glu Ala Asn Arg Ser Leu Val Leu
            180                 185                 190

Thr Glu Gly Ala Arg Ala Asp Ala Ile Pro Asn Leu Glu Ile Glu Thr
        195                 200                 205

Gly Gln Ile Val Gly Ala Gly His Ala Ala Thr Val Gly Arg Phe Asp
    210                 215                 220

Asp Glu His Val Phe Tyr Leu Gln Ala Arg Gly Ile Pro Ala Glu Glu
225                 230                 235                 240

Ala Arg Arg Leu Ile Val Arg Gly Phe Phe Asn Glu Val Ile Asn Lys
                245                 250                 255

Val Pro Val Glu Ser Ile Arg Gly Glu Leu Asp Asn Arg Val Ser Ser
            260                 265                 270

Glu Leu Ala Val Leu Gly Met
        275
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<210> 2771
<211> 534
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(511)
<223> RXA02518

<400> 2771
cgcgtgaagt gcgcgctgct tgggtggaag gctttccagg cggcaaccgc tgacgctgtt 60

gcgcacgcac attagcccgc tgtattaatt ggaggaaacc atg agc gag cac acc 115
                                                Met Ser Glu His Thr
                                                  1   5

gag aac acg aca gag gtt gaa gac cag aac gct tcc acc ttt gaa gca 163
Glu Asn Thr Thr Glu Val Glu Asp Gln Asn Ala Ser Thr Phe Glu Ala
                10   15   20

caa agc tct gag cgc cca gag cag tcc gag gca gac ctg gct aag gcc 211

```
Gln Ser Ser Glu Arg Pro Glu Gln Ser Glu Ala Asp Leu Ala Lys Ala
            25                  30                  35

agc gat gtt gag gag tac atg cgc gac gtt att gac cct gaa ctg ggc   259
Ser Asp Val Glu Glu Tyr Met Arg Asp Val Ile Asp Pro Glu Leu Gly
        40                  45                  50

att aac gtt gtt gac ctg ggc ctt gtc tac gat att tac atc atc aac   307
Ile Asn Val Val Asp Leu Gly Leu Val Tyr Asp Ile Tyr Ile Ile Asn
    55                  60                  65

ggc aac gaa gct cac atc gat atg act ctg act tca cca gct tgc ccg   355
Gly Asn Glu Ala His Ile Asp Met Thr Leu Thr Ser Pro Ala Cys Pro
70                  75                  80                  85

ctg act gac gtc atc gaa gat cag gca cgc acc gca atc gtc ggc aac   403
Leu Thr Asp Val Ile Glu Asp Gln Ala Arg Thr Ala Ile Val Gly Asn
                90                  95                  100

ggc att gca gag aag atg tcc ctg aac tgg gta tgg atg cca cct tgg   451
Gly Ile Ala Glu Lys Met Ser Leu Asn Trp Val Trp Met Pro Pro Trp
            105                 110                 115

ggt cca cac atg att acc gaa gag ggc cgc gct cag ctg cag gcc cta   499
Gly Pro His Met Ile Thr Glu Glu Gly Arg Ala Gln Leu Gln Ala Leu
        120                 125                 130

gga ttc gcg gtt taaaaggctg cttatcgacg cca                        534
Gly Phe Ala Val
    135


<210> 2772
<211> 137
<212> PRT
<213> Corynebacterium glutamicum

<400> 2772
Met Ser Glu His Thr Glu Asn Thr Thr Glu Val Glu Asp Gln Asn Ala
  1               5                  10                  15

Ser Thr Phe Glu Ala Gln Ser Ser Glu Arg Pro Glu Gln Ser Glu Ala
            20                  25                  30

Asp Leu Ala Lys Ala Ser Asp Val Glu Glu Tyr Met Arg Asp Val Ile
        35                  40                  45

Asp Pro Glu Leu Gly Ile Asn Val Val Asp Leu Gly Leu Val Tyr Asp
    50                  55                  60

Ile Tyr Ile Ile Asn Gly Asn Glu Ala His Ile Asp Met Thr Leu Thr
65                  70                  75                  80

Ser Pro Ala Cys Pro Leu Thr Asp Val Ile Glu Asp Gln Ala Arg Thr
                85                  90                  95

Ala Ile Val Gly Asn Gly Ile Ala Glu Lys Met Ser Leu Asn Trp Val
            100                 105                 110

Trp Met Pro Pro Trp Gly Pro His Met Ile Thr Glu Glu Gly Arg Ala
        115                 120                 125
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Gln Leu Gln Ala Leu Gly Phe Ala Val
    130                 135


<210> 2773
<211> 1566
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1543)
<223> RXA02521

<400> 2773
gcacacgcaa ccattggcaa caatcgcgga cggccacggc atctgcacaa caaatattgc 60

attgacaccc atcaaacact cctgatgaaa ggagcggatc atg act tcg gca acg   115
                                            Met Thr Ser Ala Thr
                                              1               5

acg aac cca ggg gtt aac gag ccc ttg acc gat gac cag atc att gaa   163
Thr Asn Pro Gly Val Asn Glu Pro Leu Thr Asp Asp Gln Ile Ile Glu
                 10                  15                  20

tcc atc ggt ccg tac aac tat ggt tgg cac gac tcc gac gac gct ggt   211
Ser Ile Gly Pro Tyr Asn Tyr Gly Trp His Asp Ser Asp Asp Ala Gly
             25                  30                  35

gca tcc gca cag cgt ggt ctc agc gag gat gtc gta cgc gac atc tct   259
Ala Ser Ala Gln Arg Gly Leu Ser Glu Asp Val Val Arg Asp Ile Ser
         40                  45                  50

gcg aag aag agc gag cca gaa tgg atg ctt cag cag cgc ctc aag gcc   307
Ala Lys Lys Ser Glu Pro Glu Trp Met Leu Gln Gln Arg Leu Lys Ala
     55                  60                  65

ctg agc att ttt gat aag aag cca gtt cca acc tgg ggt gca gac ctt   355
Leu Ser Ile Phe Asp Lys Lys Pro Val Pro Thr Trp Gly Ala Asp Leu
 70                  75                  80                  85

tca ggc att gac ttc gac aac att aaa tac ttc gtc cgc tcc act gag   403
Ser Gly Ile Asp Phe Asp Asn Ile Lys Tyr Phe Val Arg Ser Thr Glu
                 90                  95                 100

aag cag gca cag tcc tgg gag gat ctc cca gaa gac atc aag aat acc   451
Lys Gln Ala Gln Ser Trp Glu Asp Leu Pro Glu Asp Ile Lys Asn Thr
            105                 110                 115

tac gac aag ctg ggt att cct gag gcc gag aag cag cgc ctc gtt gca   499
Tyr Asp Lys Leu Gly Ile Pro Glu Ala Glu Lys Gln Arg Leu Val Ala
        120                 125                 130

ggt gtt gca gct cag tac gag tct gag gtt gtc tac cac cag atc cgc   547
Gly Val Ala Ala Gln Tyr Glu Ser Glu Val Val Tyr His Gln Ile Arg
    135                 140                 145

gag gac ctg gag gaa aag gga gtt atc ttc ctt gac acc gat acc gca   595
Glu Asp Leu Glu Glu Lys Gly Val Ile Phe Leu Asp Thr Asp Thr Ala
150                 155                 160                 165
```

```
ctg aaa gag cac cct gag atc ttc cag gag tac ttc ggc acc gtc att   643
Leu Lys Glu His Pro Glu Ile Phe Gln Glu Tyr Phe Gly Thr Val Ile
                170                 175                 180

cca gca ggc gac aac aag ttc tcc gca ctg aac tcc gct gtc tgg tcc   691
Pro Ala Gly Asp Asn Lys Phe Ser Ala Leu Asn Ser Ala Val Trp Ser
            185                 190                 195

ggt gga tct ttc atc tac gtg cca aag ggt gtc cac gtg gac att cct   739
Gly Gly Ser Phe Ile Tyr Val Pro Lys Gly Val His Val Asp Ile Pro
        200                 205                 210

ctg cag gct tac ttc cgc atc aac acc gag aac atg ggt cag ttc gaa   787
Leu Gln Ala Tyr Phe Arg Ile Asn Thr Glu Asn Met Gly Gln Phe Glu
    215                 220                 225

cgc acc ctg atc atc gtt gat gag gat gcc tac gtt cac tac gtt gag   835
Arg Thr Leu Ile Ile Val Asp Glu Asp Ala Tyr Val His Tyr Val Glu
230                 235                 240                 245

ggc tgt acc gca cct att tac aag tcc gac tcc ctg cac tcc gca gtc   883
Gly Cys Thr Ala Pro Ile Tyr Lys Ser Asp Ser Leu His Ser Ala Val
                250                 255                 260

gtt gag atc atc gtg aag aag ggt gga cgc tgc cgc tac acc acc att   931
Val Glu Ile Ile Val Lys Lys Gly Gly Arg Cys Arg Tyr Thr Thr Ile
            265                 270                 275

cag aac tgg tcc aac aac gtc tac aac ctg gtg acc aag cgc acc aag   979
Gln Asn Trp Ser Asn Asn Val Tyr Asn Leu Val Thr Lys Arg Thr Lys
        280                 285                 290

gtt gaa gag ggc ggc acc atg gaa tgg gtc gat ggc aac atc ggc tcc   1027
Val Glu Glu Gly Gly Thr Met Glu Trp Val Asp Gly Asn Ile Gly Ser
    295                 300                 305

aag gtc acc atg aag tac cca gct gtc tgg atg act ggc cca cac gca   1075
Lys Val Thr Met Lys Tyr Pro Ala Val Trp Met Thr Gly Pro His Ala
310                 315                 320                 325

aag ggc gaa gtt ctc tcc gtc gct ttc gca ggt gag gga cag ttc cag   1123
Lys Gly Glu Val Leu Ser Val Ala Phe Ala Gly Glu Gly Gln Phe Gln
                330                 335                 340

gac acc ggc gcc aag atg acc cac atg gct cct tac act tcc tcc aac   1171
Asp Thr Gly Ala Lys Met Thr His Met Ala Pro Tyr Thr Ser Ser Asn
            345                 350                 355

atc gtg tcc aag tct gtg gca cgt ggc ggt gga cgt gcg gct tac cgt   1219
Ile Val Ser Lys Ser Val Ala Arg Gly Gly Gly Arg Ala Ala Tyr Arg
        360                 365                 370

ggt ctg gtt cag atc aac gca aac gct cac cac tca acc tcc aac gtt   1267
Gly Leu Val Gln Ile Asn Ala Asn Ala His His Ser Thr Ser Asn Val
    375                 380                 385

gag tgt gac gca ctg ctg gtc gat gac atc tcc cgt tct gac acc tac   1315
Glu Cys Asp Ala Leu Leu Val Asp Asp Ile Ser Arg Ser Asp Thr Tyr
390                 395                 400                 405
```

```
cca tac aac gac atc cgt aac gat cac gtg tca ctc ggc cac gag gca   1363
Pro Tyr Asn Asp Ile Arg Asn Asp His Val Ser Leu Gly His Glu Ala
                410                 415                 420

act gtt tcc cag gtt tct gaa gag cag ctg ttc tac ctc atg agc cgc   1411
Thr Val Ser Gln Val Ser Glu Glu Gln Leu Phe Tyr Leu Met Ser Arg
            425                 430                 435

gga ctt gcg gaa gaa gaa gca atg gca atg atc gtt cgt ggc ttc gtt   1459
Gly Leu Ala Glu Glu Glu Ala Met Ala Met Ile Val Arg Gly Phe Val
        440                 445                 450

gag cca atc gct aag gaa ctc cca atg gag tac gcc ctt gag ctc aac   1507
Glu Pro Ile Ala Lys Glu Leu Pro Met Glu Tyr Ala Leu Glu Leu Asn
    455                 460                 465

cga ctg atc gaa ctg cag atg gaa gga tcg gtg ggc taagcccaat        1553
Arg Leu Ile Glu Leu Gln Met Glu Gly Ser Val Gly
470                 475                 480

gactgaagta gca                                                   1566
```

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<210> 2774
<211> 481
<212> PRT
<213> Corynebacterium glutamicum

<400> 2774

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Met Thr Ser Ala Thr Thr Asn Pro Gly Val Asn Glu Pro Leu Thr Asp
  1               5                  10                  15

Asp Gln Ile Ile Glu Ser Ile Gly Pro Tyr Asn Tyr Gly Trp His Asp
             20                  25                  30

Ser Asp Asp Ala Gly Ala Ser Ala Gln Arg Gly Leu Ser Glu Asp Val
         35                  40                  45

Val Arg Asp Ile Ser Ala Lys Lys Ser Glu Pro Glu Trp Met Leu Gln
     50                  55                  60

Gln Arg Leu Lys Ala Leu Ser Ile Phe Asp Lys Lys Pro Val Pro Thr
 65                  70                  75                  80

Trp Gly Ala Asp Leu Ser Gly Ile Asp Phe Asp Asn Ile Lys Tyr Phe
                 85                  90                  95

Val Arg Ser Thr Glu Lys Gln Ala Gln Ser Trp Glu Asp Leu Pro Glu
            100                 105                 110

Asp Ile Lys Asn Thr Tyr Asp Lys Leu Gly Ile Pro Glu Ala Glu Lys
        115                 120                 125

Gln Arg Leu Val Ala Gly Val Ala Ala Gln Tyr Glu Ser Glu Val Val
    130                 135                 140

Tyr His Gln Ile Arg Glu Asp Leu Glu Glu Lys Gly Val Ile Phe Leu
145                 150                 155                 160

Asp Thr Asp Thr Ala Leu Lys Glu His Pro Glu Ile Phe Gln Glu Tyr
                165                 170                 175
```

```
Phe Gly Thr Val Ile Pro Ala Gly Asp Asn Lys Phe Ser Ala Leu Asn
            180                 185                 190

Ser Ala Val Trp Ser Gly Gly Ser Phe Ile Tyr Val Pro Lys Gly Val
        195                 200                 205

His Val Asp Ile Pro Leu Gln Ala Tyr Phe Arg Ile Asn Thr Glu Asn
    210                 215                 220

Met Gly Gln Phe Glu Arg Thr Leu Ile Ile Val Asp Glu Asp Ala Tyr
225                 230                 235                 240

Val His Tyr Val Glu Gly Cys Thr Ala Pro Ile Tyr Lys Ser Asp Ser
                245                 250                 255

Leu His Ser Ala Val Val Glu Ile Ile Val Lys Lys Gly Gly Arg Cys
            260                 265                 270

Arg Tyr Thr Thr Ile Gln Asn Trp Ser Asn Asn Val Tyr Asn Leu Val
        275                 280                 285

Thr Lys Arg Thr Lys Val Glu Glu Gly Gly Thr Met Glu Trp Val Asp
    290                 295                 300

Gly Asn Ile Gly Ser Lys Val Thr Met Lys Tyr Pro Ala Val Trp Met
305                 310                 315                 320

Thr Gly Pro His Ala Lys Gly Glu Val Leu Ser Val Ala Phe Ala Gly
                325                 330                 335

Glu Gly Gln Phe Gln Asp Thr Gly Ala Lys Met Thr His Met Ala Pro
            340                 345                 350

Tyr Thr Ser Ser Asn Ile Val Ser Lys Ser Val Ala Arg Gly Gly Gly
        355                 360                 365

Arg Ala Ala Tyr Arg Gly Leu Val Gln Ile Asn Ala Asn Ala His His
    370                 375                 380

Ser Thr Ser Asn Val Glu Cys Asp Ala Leu Leu Val Asp Asp Ile Ser
385                 390                 395                 400

Arg Ser Asp Thr Tyr Pro Tyr Asn Asp Ile Arg Asn Asp His Val Ser
                405                 410                 415

Leu Gly His Glu Ala Thr Val Ser Gln Val Ser Glu Glu Gln Leu Phe
            420                 425                 430

Tyr Leu Met Ser Arg Gly Leu Ala Glu Glu Glu Ala Met Ala Met Ile
        435                 440                 445

Val Arg Gly Phe Val Glu Pro Ile Ala Lys Glu Leu Pro Met Glu Tyr
    450                 455                 460

Ala Leu Glu Leu Asn Arg Leu Ile Glu Leu Gln Met Glu Gly Ser Val
465                 470                 475                 480

Gly
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<210> 2775
<211> 813
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(790)
<223> RXA02524

<400> 2775
gacgcgatca ggcgctccta cgcacccagg caattaggcc tgagcttatc gacgcatccc 60

tcctcgattc caccgacctc aaagtattgg gactggacaa atg aca gag acc aca 115
Met Thr Glu Thr Thr
1 5

cct caa ccc cca aag cca gag ccc gag ctc ccg aaa ttt ctc agc aac 163
Pro Gln Pro Pro Lys Pro Glu Pro Glu Leu Pro Lys Phe Leu Ser Asn
10 15 20

cca gaa cgc gcc gac atc att ttg ttc atc gca ctc att gtg atg ggc 211
Pro Glu Arg Ala Asp Ile Ile Leu Phe Ile Ala Leu Ile Val Met Gly
25 30 35

att ttc tcc ctc tgc atg atc cca ctg cgc gcc tgg atg ctc acc caa 259
Ile Phe Ser Leu Cys Met Ile Pro Leu Arg Ala Trp Met Leu Thr Gln
40 45 50

cct ctg gcc tac acc ctc atc gtc ggt ggt tac acc agt gca gtc gtg 307
Pro Leu Ala Tyr Thr Leu Ile Val Gly Gly Tyr Thr Ser Ala Val Val
55 60 65

ggc ggc gcg aac gct tcg gta gaa aac ggc atc tgg tgg gtc tac tgg 355
Gly Gly Ala Asn Ala Ser Val Glu Asn Gly Ile Trp Trp Val Tyr Trp
70 75 80 85

ctc tgc acc ctg atc ggc gcg ctg aag ttc atg ccc gtc tat tgg ctg 403
Leu Cys Thr Leu Ile Gly Ala Leu Lys Phe Met Pro Val Tyr Trp Leu
90 95 100

atg ggt aag cgc tgg ggc atg gaa ttt atc gac atg tcc ctc caa tac 451
Met Gly Lys Arg Trp Gly Met Glu Phe Ile Asp Met Ser Leu Gln Tyr
105 110 115

atg ccc cgc ttc cac cgc atg ttc aaa aaa tcc gtc gac tcc gaa tcc 499
Met Pro Arg Phe His Arg Met Phe Lys Lys Ser Val Asp Ser Glu Ser
120 125 130

acc cgc ctc tac gcc tgg atc atc ggc ctc att cca ctc gca tac ctc 547
Thr Arg Leu Tyr Ala Trp Ile Ile Gly Leu Ile Pro Leu Ala Tyr Leu
135 140 145

cca gga cca gtg ccg gga acc atc ctt aac gca gtg gct ggg ctg gtg 595
Pro Gly Pro Val Pro Gly Thr Ile Leu Asn Ala Val Ala Gly Leu Val
150 155 160 165

aaa atc ccc ttc tgg atc atc atg gcc tgg aat gcg atc tgc gta cta 643
Lys Ile Pro Phe Trp Ile Ile Met Ala Trp Asn Ala Ile Cys Val Leu
170 175 180

```
tcg gtc aac gga cta ttc atg tgg ctg gga tac acc ttc ggc gaa caa   691
Ser Val Asn Gly Leu Phe Met Trp Leu Gly Tyr Thr Phe Gly Glu Gln
            185                 190                 195

gtc ctc gac atc gtc aac gtg gtc aac cgc tac atg ctt tgg ata acc   739
Val Leu Asp Ile Val Asn Val Val Asn Arg Tyr Met Leu Trp Ile Thr
        200                 205                 210

tta gga ttg ctg gcg ctg atg ttt ttc cgc gca cgg aag caa ttt gcc   787
Leu Gly Leu Leu Ala Leu Met Phe Phe Arg Ala Arg Lys Gln Phe Ala
    215                 220                 225

aag taaatggttg aaaggaatat gac                                    813
Lys
230
```

<210> 2776
<211> 230
<212> PRT
<213> Corynebacterium glutamicum

<400> 2776

```
Met Thr Glu Thr Thr Pro Gln Pro Pro Lys Pro Glu Pro Glu Leu Pro
  1               5                  10                  15

Lys Phe Leu Ser Asn Pro Glu Arg Ala Asp Ile Ile Leu Phe Ile Ala
             20                  25                  30

Leu Ile Val Met Gly Ile Phe Ser Leu Cys Met Ile Pro Leu Arg Ala
         35                  40                  45

Trp Met Leu Thr Gln Pro Leu Ala Tyr Thr Leu Ile Val Gly Gly Tyr
     50                  55                  60

Thr Ser Ala Val Val Gly Gly Ala Asn Ala Ser Val Glu Asn Gly Ile
 65                  70                  75                  80

Trp Trp Val Tyr Trp Leu Cys Thr Leu Ile Gly Ala Leu Lys Phe Met
                 85                  90                  95

Pro Val Tyr Trp Leu Met Gly Lys Arg Trp Gly Met Glu Phe Ile Asp
            100                 105                 110

Met Ser Leu Gln Tyr Met Pro Arg Phe His Arg Met Phe Lys Lys Ser
        115                 120                 125

Val Asp Ser Glu Ser Thr Arg Leu Tyr Ala Trp Ile Ile Gly Leu Ile
    130                 135                 140

Pro Leu Ala Tyr Leu Pro Gly Pro Val Pro Gly Thr Ile Leu Asn Ala
145                 150                 155                 160

Val Ala Gly Leu Val Lys Ile Pro Phe Trp Ile Ile Met Ala Trp Asn
                165                 170                 175

Ala Ile Cys Val Leu Ser Val Asn Gly Leu Phe Met Trp Leu Gly Tyr
            180                 185                 190

Thr Phe Gly Glu Gln Val Leu Asp Ile Val Asn Val Val Asn Arg Tyr
```

```
        195                 200                 205

Met Leu Trp Ile Thr Leu Gly Leu Leu Ala Leu Met Phe Phe Arg Ala
    210                 215                 220

Arg Lys Gln Phe Ala Lys
225                 230


<210> 2777
<211> 501
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(478)
<223> RXA02525

<400> 2777
cgtggtcaac cgctacatgc tttggataac cttaggattg ctggcgctga tgtttttccg 60

cgcacggaag caatttgcca agtaaatggt tgaaaggaat atg acc acc atg cga   115
                                            Met Thr Thr Met Arg
                                              1               5

gaa gtt tca acc gac ctc aac atc ctc atc gtc ccc agc gaa tgg gaa   163
Glu Val Ser Thr Asp Leu Asn Ile Leu Ile Val Pro Ser Glu Trp Glu
                 10                  15                  20

aaa gta cta gaa aac cta cca gcg aca ttg agt gag tcc gga ttc gta   211
Lys Val Leu Glu Asn Leu Pro Ala Thr Leu Ser Glu Ser Gly Phe Val
             25                  30                  35

gcc tct gaa atc cac tcc cag atc gtc gac ctc acc tgc gaa ccc gac   259
Ala Ser Glu Ile His Ser Gln Ile Val Asp Leu Thr Cys Glu Pro Asp
         40                  45                  50

aac atg ctt gtc acc cag ttc tcc cag cta gag ggc cac cca cca att   307
Asn Met Leu Val Thr Gln Phe Ser Gln Leu Glu Gly His Pro Pro Ile
     55                  60                  65

gtg gaa gtg ctc cac cgc cta gta att aac ggc tcc tcc gac ctg gag   355
Val Glu Val Leu His Arg Leu Val Ile Asn Gly Ser Ser Asp Leu Glu
 70                  75                  80                  85

ctt aaa gac ctc acc aaa aag gtg gtg ggg gcg ttg cct cag ggg acc   403
Leu Lys Asp Leu Thr Lys Lys Val Val Gly Ala Leu Pro Gln Gly Thr
                 90                  95                 100

tac tgg tat gga act tcc ctt gaa ggt gcg acc gaa cct ggc gtt aac   451
Tyr Trp Tyr Gly Thr Ser Leu Glu Gly Ala Thr Glu Pro Gly Val Asn
            105                 110                 115

gca tca tgc gcg tgg cag cat cgg ggc tagttttccg cgtttagtca         498
Ala Ser Cys Ala Trp Gln His Arg Gly
        120                 125

gtt                                                               501
```

<210> 2778
<211> 126
<212> PRT
<213> Corynebacterium glutamicum

<400> 2778
Met Thr Thr Met Arg Glu Val Ser Thr Asp Leu Asn Ile Leu Ile Val
1 5 10 15

Pro Ser Glu Trp Glu Lys Val Leu Glu Asn Leu Pro Ala Thr Leu Ser
20 25 30

Glu Ser Gly Phe Val Ala Ser Glu Ile His Ser Gln Ile Val Asp Leu
35 40 45

Thr Cys Glu Pro Asp Asn Met Leu Val Thr Gln Phe Ser Gln Leu Glu
50 55 60

Gly His Pro Pro Ile Val Glu Val Leu His Arg Leu Val Ile Asn Gly
65 70 75 80

Ser Ser Asp Leu Glu Leu Lys Asp Leu Thr Lys Lys Val Val Gly Ala
85 90 95

Leu Pro Gln Gly Thr Tyr Trp Tyr Gly Thr Ser Leu Glu Gly Ala Thr
100 105 110

Glu Pro Gly Val Asn Ala Ser Cys Ala Trp Gln His Arg Gly
115 120 125

<210> 2779
<211> 561
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(538)
<223> RXA02540

<400> 2779
gcatatgctg aagcagaaac taattcaggt tttgatcccc gcgctaactg ggcgggccag 60

aaccgctaga cgttctcttt gagaaaggag gtgacgaaac atg gca tcc aca ccg 115
Met Ala Ser Thr Pro
1 5

aaa aaa tcc aac gat gaa ggt cag ttt gac cgt gtc gat ttt caa ggg 163
Lys Lys Ser Asn Asp Glu Gly Gln Phe Asp Arg Val Asp Phe Gln Gly
10 15 20

gaa gtc ttc gtt atc tct gtc gca gcc gag ctt gcc ggc atg cat gcc 211
Glu Val Phe Val Ile Ser Val Ala Ala Glu Leu Ala Gly Met His Ala
25 30 35

caa act ttg cga acc tac gat cgc atg ggt ttg gtc acc ccg ata cgc 259
Gln Thr Leu Arg Thr Tyr Asp Arg Met Gly Leu Val Thr Pro Ile Arg
40 45 50

act cgc gga ggc ggt cgc cgt tac tcc cgc gct gac gtg gaa tta ctc 307

```
Thr Arg Gly Gly Gly Arg Arg Tyr Ser Arg Ala Asp Val Glu Leu Leu
     55                  60                  65

cga gaa att cag cac ctc agc cag gag gaa ggc gta aac ctc gcc gga   355
Arg Glu Ile Gln His Leu Ser Gln Glu Glu Gly Val Asn Leu Ala Gly
 70                  75                  80                  85

atc aag gcg atc atc gag ctc ggc gaa gaa aac cga aac ctc aaa gaa   403
Ile Lys Ala Ile Ile Glu Leu Gly Glu Glu Asn Arg Asn Leu Lys Glu
                90                  95                 100

tcc ctg cgt aag gtc aca gct gag aat gag cag ctc aaa gat caa tta   451
Ser Leu Arg Lys Val Thr Ala Glu Asn Glu Gln Leu Lys Asp Gln Leu
            105                 110                 115

cgc agc ggg cgt ccg cgt ggc gag ctg gtg cac gtg ccc cgc tcc acc   499
Arg Ser Gly Arg Pro Arg Gly Glu Leu Val His Val Pro Arg Ser Thr
        120                 125                 130

gcg gtg gtc atg tgg gaa cgc cgc aag ggg cgt tcc aag taaaaacatg    548
Ala Val Val Met Trp Glu Arg Arg Lys Gly Arg Ser Lys
    135                 140                 145

cttgtcgacg cca                                                   561


<210> 2780
<211> 146
<212> PRT
<213> Corynebacterium glutamicum

<400> 2780
Met Ala Ser Thr Pro Lys Lys Ser Asn Asp Glu Gly Gln Phe Asp Arg
  1               5                  10                  15

Val Asp Phe Gln Gly Glu Val Phe Val Ile Ser Val Ala Ala Glu Leu
             20                  25                  30

Ala Gly Met His Ala Gln Thr Leu Arg Thr Tyr Asp Arg Met Gly Leu
         35                  40                  45

Val Thr Pro Ile Arg Thr Arg Gly Gly Gly Arg Arg Tyr Ser Arg Ala
     50                  55                  60

Asp Val Glu Leu Leu Arg Glu Ile Gln His Leu Ser Gln Glu Glu Gly
 65                  70                  75                  80

Val Asn Leu Ala Gly Ile Lys Ala Ile Ile Glu Leu Gly Glu Glu Asn
                 85                  90                  95

Arg Asn Leu Lys Glu Ser Leu Arg Lys Val Thr Ala Glu Asn Glu Gln
            100                 105                 110

Leu Lys Asp Gln Leu Arg Ser Gly Arg Pro Arg Gly Glu Leu Val His
        115                 120                 125

Val Pro Arg Ser Thr Ala Val Val Met Trp Glu Arg Arg Lys Gly Arg
    130                 135                 140

Ser Lys
145
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<210> 2781
<211> 1551
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1528)
<223> RXA02544

<400> 2781
ccaatcaggg aagataagag ctgttttcaa caggtcccac tcaactttga caccaagtct 60

cacgcaaaat taacagccat aaactttaga aggacaccct gtg tcc cac acc tgt 115
Val Ser His Thr Cys
1 5

ggc ata gtg att ttt gtg agc aca gaa tca gga aac acc cca aaa agg 163
Gly Ile Val Ile Phe Val Ser Thr Glu Ser Gly Asn Thr Pro Lys Arg
10 15 20

gat gat gca aaa agc acc atc cct ccg aaa gat ttg cct gac acc gtc 211
Asp Asp Ala Lys Ser Thr Ile Pro Pro Lys Asp Leu Pro Asp Thr Val
25 30 35

tta gac gcg att gaa ggc aat ttt gag cca ccg cta aat acc cag aag 259
Leu Asp Ala Ile Glu Gly Asn Phe Glu Pro Pro Leu Asn Thr Gln Lys
40 45 50

tcg gcg gtt ccc cct aat gcc gaa gca act gtc gag gct gat tct gaa 307
Ser Ala Val Pro Pro Asn Ala Glu Ala Thr Val Glu Ala Asp Ser Glu
55 60 65

gga act acc gac cgc tct gtc att ttg ggc agg gac ggc cgc tgg ctg 355
Gly Thr Thr Asp Arg Ser Val Ile Leu Gly Arg Asp Gly Arg Trp Leu
70 75 80 85

tcc gga tgg gca ttg cgc ttc atc gtg ctg gtt atc gcc ggc gtc att 403
Ser Gly Trp Ala Leu Arg Phe Ile Val Leu Val Ile Ala Gly Val Ile
90 95 100

gca ctt cgt atg ctg ggc ttc atc tgg gtt ggc atc ctc cca gtc gtc 451
Ala Leu Arg Met Leu Gly Phe Ile Trp Val Gly Ile Leu Pro Val Val
105 110 115

ctc gca ctt cta gtc tgc acc gtg cta tgg cca cca gtg aaa tgg ctg 499
Leu Ala Leu Leu Val Cys Thr Val Leu Trp Pro Pro Val Lys Trp Leu
120 125 130

cgc gag cat aag att ccc acg gcg ctc gcc gtt gtc atc aca att ttg 547
Arg Glu His Lys Ile Pro Thr Ala Leu Ala Val Val Ile Thr Ile Leu
135 140 145

ggt ttc ttc gcc ctc atc ggc gga gtt ttt gca gcc atc gcg cca agc 595
Gly Phe Phe Ala Leu Ile Gly Gly Val Phe Ala Ala Ile Ala Pro Ser
150 155 160 165

gtg tct tcc cag aca aag caa gtg gta gac caa gca act gtt ggt atc 643
Val Ser Ser Gln Thr Lys Gln Val Val Asp Gln Ala Thr Val Gly Ile

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                170                 175                 180

gaa gat cta atg gat tgg gtt cag ggc cca cct ttt aac tta gat atc   691
Glu Asp Leu Met Asp Trp Val Gln Gly Pro Pro Phe Asn Leu Asp Ile
            185                 190                 195

tca cag ttt gaa ggc gcg ctc aat gac cta aca tcc atg ctg caa tca   739
Ser Gln Phe Glu Gly Ala Leu Asn Asp Leu Thr Ser Met Leu Gln Ser
        200                 205                 210

cag tct tcc acc att gct tct ggt gtg ttc tct gga ctg tca acg gca   787
Gln Ser Ser Thr Ile Ala Ser Gly Val Phe Ser Gly Leu Ser Thr Ala
    215                 220                 225

tca tcc atc gtt gtc aca cta gca gtg atg ctg gtg ttg acc ttc ttc   835
Ser Ser Ile Val Val Thr Leu Ala Val Met Leu Val Leu Thr Phe Phe
230                 235                 240                 245

ttc ctc aaa gac ggt cct cgt ttc ctg cca tgg atg cgc ggc ttc act   883
Phe Leu Lys Asp Gly Pro Arg Phe Leu Pro Trp Met Arg Gly Phe Thr
                250                 255                 260

ggt gaa aac gca ggt tgg cac ctc aca gaa gtc ctg acc cgt acc tgg   931
Gly Glu Asn Ala Gly Trp His Leu Thr Glu Val Leu Thr Arg Thr Trp
            265                 270                 275

aat acc ttg gcc gga ttc atc cgt gct cag gca ttg gtg tcc atg gtt   979
Asn Thr Leu Ala Gly Phe Ile Arg Ala Gln Ala Leu Val Ser Met Val
        280                 285                 290

gac gca ata ttc att ggt atc gga ttg ctg ctt ctt ggc gtc cca atg   1027
Asp Ala Ile Phe Ile Gly Ile Gly Leu Leu Leu Leu Gly Val Pro Met
    295                 300                 305

gcc ctc gcg ctc gcg gtc atc aca ttc ttc gcg ggc ttc atc ccc atc   1075
Ala Leu Ala Leu Ala Val Ile Thr Phe Phe Ala Gly Phe Ile Pro Ile
310                 315                 320                 325

gtc ggt gcg gtg tct gca ggc gcc ctg gct gtc atc atc gcg cta gtt   1123
Val Gly Ala Val Ser Ala Gly Ala Leu Ala Val Ile Ile Ala Leu Val
                330                 335                 340

acc aac ggc gtg acc aat gcg ctt ttg gta ctt gta ttg atc ctg gcg   1171
Thr Asn Gly Val Thr Asn Ala Leu Leu Val Leu Val Leu Ile Leu Ala
            345                 350                 355

gtt cag cag atc gag ggc aat atc ttg tcc cca ttc ctg cag tcc aag   1219
Val Gln Gln Ile Glu Gly Asn Ile Leu Ser Pro Phe Leu Gln Ser Lys
        360                 365                 370

gct atg aac ctg cac gca gcg gtt gtt ttg cta tcc gtc acc gtc ggc   1267
Ala Met Asn Leu His Ala Ala Val Val Leu Leu Ser Val Thr Val Gly
    375                 380                 385

tcc acc atg ttc ggc atc atc ggc gca ttc ttg gct gtt cca gta gcc   1315
Ser Thr Met Phe Gly Ile Ile Gly Ala Phe Leu Ala Val Pro Val Ala
390                 395                 400                 405

gcg acg ttg gct gtc tgg gtg cgc tac cac tct gaa atg gtt gct ttg   1363
Ala Thr Leu Ala Val Trp Val Arg Tyr His Ser Glu Met Val Ala Leu
                410                 415                 420
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cgc gcc ggt gag atc acc agt gat gac att gag atc gcc acg acg aaa   1411
Arg Ala Gly Glu Ile Thr Ser Asp Asp Ile Glu Ile Ala Thr Thr Lys
            425                 430                 435

ggt tcc cca acc agc ctc aat ggc caa gaa acc ctt gct gcc att cga   1459
Gly Ser Pro Thr Ser Leu Asn Gly Gln Glu Thr Leu Ala Ala Ile Arg
        440                 445                 450

agc aga ttc gcc atc ctt ggc cgc aag aag ccg aca tct gcc act gca   1507
Ser Arg Phe Ala Ile Leu Gly Arg Lys Lys Pro Thr Ser Ala Thr Ala
    455                 460                 465

gaa aaa gca gac tca gaa agc tagccaataa tgctcactcc cga             1551
Glu Lys Ala Asp Ser Glu Ser
470                 475
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<210> 2782
<211> 476
<212> PRT
<213> Corynebacterium glutamicum

<400> 2782

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Val Ser His Thr Cys Gly Ile Val Ile Phe Val Ser Thr Glu Ser Gly
  1               5                  10                  15

Asn Thr Pro Lys Arg Asp Asp Ala Lys Ser Thr Ile Pro Pro Lys Asp
             20                  25                  30

Leu Pro Asp Thr Val Leu Asp Ala Ile Glu Gly Asn Phe Glu Pro Pro
         35                  40                  45

Leu Asn Thr Gln Lys Ser Ala Val Pro Pro Asn Ala Glu Ala Thr Val
     50                  55                  60

Glu Ala Asp Ser Glu Gly Thr Thr Asp Arg Ser Val Ile Leu Gly Arg
 65                  70                  75                  80

Asp Gly Arg Trp Leu Ser Gly Trp Ala Leu Arg Phe Ile Val Leu Val
                 85                  90                  95

Ile Ala Gly Val Ile Ala Leu Arg Met Leu Gly Phe Ile Trp Val Gly
            100                 105                 110

Ile Leu Pro Val Val Leu Ala Leu Leu Val Cys Thr Val Leu Trp Pro
        115                 120                 125

Pro Val Lys Trp Leu Arg Glu His Lys Ile Pro Thr Ala Leu Ala Val
    130                 135                 140

Val Ile Thr Ile Leu Gly Phe Phe Ala Leu Ile Gly Gly Val Phe Ala
145                 150                 155                 160

Ala Ile Ala Pro Ser Val Ser Ser Gln Thr Lys Gln Val Val Asp Gln
                165                 170                 175

Ala Thr Val Gly Ile Glu Asp Leu Met Asp Trp Val Gln Gly Pro Pro
            180                 185                 190

Phe Asn Leu Asp Ile Ser Gln Phe Glu Gly Ala Leu Asn Asp Leu Thr
```

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        195                 200                 205

Ser Met Leu Gln Ser Gln Ser Ser Thr Ile Ala Ser Gly Val Phe Ser
    210                 215                 220

Gly Leu Ser Thr Ala Ser Ser Ile Val Val Thr Leu Ala Val Met Leu
225                 230                 235                 240

Val Leu Thr Phe Phe Phe Leu Lys Asp Gly Pro Arg Phe Leu Pro Trp
                245                 250                 255

Met Arg Gly Phe Thr Gly Glu Asn Ala Gly Trp His Leu Thr Glu Val
            260                 265                 270

Leu Thr Arg Thr Trp Asn Thr Leu Ala Gly Phe Ile Arg Ala Gln Ala
        275                 280                 285

Leu Val Ser Met Val Asp Ala Ile Phe Ile Gly Ile Gly Leu Leu Leu
    290                 295                 300

Leu Gly Val Pro Met Ala Leu Ala Leu Ala Val Ile Thr Phe Phe Ala
305                 310                 315                 320

Gly Phe Ile Pro Ile Val Gly Ala Val Ser Ala Gly Ala Leu Ala Val
                325                 330                 335

Ile Ile Ala Leu Val Thr Asn Gly Val Thr Asn Ala Leu Leu Val Leu
            340                 345                 350

Val Leu Ile Leu Ala Val Gln Gln Ile Glu Gly Asn Ile Leu Ser Pro
        355                 360                 365

Phe Leu Gln Ser Lys Ala Met Asn Leu His Ala Ala Val Val Leu Leu
    370                 375                 380

Ser Val Thr Val Gly Ser Thr Met Phe Gly Ile Ile Gly Ala Phe Leu
385                 390                 395                 400

Ala Val Pro Val Ala Ala Thr Leu Ala Val Trp Val Arg Tyr His Ser
                405                 410                 415

Glu Met Val Ala Leu Arg Ala Gly Glu Ile Thr Ser Asp Asp Ile Glu
            420                 425                 430

Ile Ala Thr Thr Lys Gly Ser Pro Thr Ser Leu Asn Gly Gln Glu Thr
        435                 440                 445

Leu Ala Ala Ile Arg Ser Arg Phe Ala Ile Leu Gly Arg Lys Lys Pro
    450                 455                 460

Thr Ser Ala Thr Ala Glu Lys Ala Asp Ser Glu Ser
465                 470                 475


<210> 2783
<211> 681
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
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<222> (101)..(658)
<223> RXA02545

<400> 2783
aagaaatcga gaaagtaatt cgtgggtgaa gttgtttcag agttgttttt tattaaacaa 60

ctcagcctgt aacctcttgg tcgttctatg cttggtcacc atg act gag act ctt 115
Met Thr Glu Thr Leu
1 5

ttt gta tcc gcc aca act gag gaa gcg gtg tat ctt cca gat gga atc 163
Phe Val Ser Ala Thr Thr Glu Glu Ala Val Tyr Leu Pro Asp Gly Ile
10 15 20

gac ttg ctg gtg act ggc atc gga acg acc gca gca acg atg att ttg 211
Asp Leu Leu Val Thr Gly Ile Gly Thr Thr Ala Ala Thr Met Ile Leu
25 30 35

act aag gag ttg gct act cgg gag gtg ctt cct gcc cga att gtc aat 259
Thr Lys Glu Leu Ala Thr Arg Glu Val Leu Pro Ala Arg Ile Val Asn
40 45 50

att ggt acg gcg gga gct ttg gtg gat gga ttg gct ggc gta tac gag 307
Ile Gly Thr Ala Gly Ala Leu Val Asp Gly Leu Ala Gly Val Tyr Glu
55 60 65

atc gaa tac gtt ctg cag cat gat ttc agt agc gag tta atc gct gaa 355
Ile Glu Tyr Val Leu Gln His Asp Phe Ser Ser Glu Leu Ile Ala Glu
70 75 80 85

atg aca gga aag cca tgc tca aat ggt tca act ttg gcc acg agt ggg 403
Met Thr Gly Lys Pro Cys Ser Asn Gly Ser Thr Leu Ala Thr Ser Gly
90 95 100

cac ttc cca gta gcg agt ttg gca aca gga aac tca ttt att gca gat 451
His Phe Pro Val Ala Ser Leu Ala Thr Gly Asn Ser Phe Ile Ala Asp
105 110 115

tca gaa acc cgc aac cac ctg gcc acc cgg gcc tcc ctc tgc gat atg 499
Ser Glu Thr Arg Asn His Leu Ala Thr Arg Ala Ser Leu Cys Asp Met
120 125 130

gag ggc gcg gcg ctg gtg ggc gtc gca aag cat ttt ggt gtt ccg att 547
Glu Gly Ala Ala Leu Val Gly Val Ala Lys His Phe Gly Val Pro Ile
135 140 145

acg ctg ctg aag cag gtt agt gac agc gcg gat gag gag gct tcg ggg 595
Thr Leu Leu Lys Gln Val Ser Asp Ser Ala Asp Glu Glu Ala Ser Gly
150 155 160 165

tcg tgg ttt gat gcg gtc gat gcg ggc gca cga cag ttg gcg gag gct 643
Ser Trp Phe Asp Ala Val Asp Ala Gly Ala Arg Gln Leu Ala Glu Ala
170 175 180

gtg aag gag ttt aaa taacaaaaac ccgatgcctg gcg 681
Val Lys Glu Phe Lys
185

<210> 2784
<211> 186

<212> PRT
<213> Corynebacterium glutamicum

<400> 2784
Met Thr Glu Thr Leu Phe Val Ser Ala Thr Thr Glu Glu Ala Val Tyr
1 5 10 15

Leu Pro Asp Gly Ile Asp Leu Leu Val Thr Gly Ile Gly Thr Thr Ala
20 25 30

Ala Thr Met Ile Leu Thr Lys Glu Leu Ala Thr Arg Glu Val Leu Pro
35 40 45

Ala Arg Ile Val Asn Ile Gly Thr Ala Gly Ala Leu Val Asp Gly Leu
50 55 60

Ala Gly Val Tyr Glu Ile Glu Tyr Val Leu Gln His Asp Phe Ser Ser
65 70 75 80

Glu Leu Ile Ala Glu Met Thr Gly Lys Pro Cys Ser Asn Gly Ser Thr
85 90 95

Leu Ala Thr Ser Gly His Phe Pro Val Ala Ser Leu Ala Thr Gly Asn
100 105 110

Ser Phe Ile Ala Asp Ser Glu Thr Arg Asn His Leu Ala Thr Arg Ala
115 120 125

Ser Leu Cys Asp Met Glu Gly Ala Ala Leu Val Gly Val Ala Lys His
130 135 140

Phe Gly Val Pro Ile Thr Leu Leu Lys Gln Val Ser Asp Ser Ala Asp
145 150 155 160

Glu Glu Ala Ser Gly Ser Trp Phe Asp Ala Val Asp Ala Gly Ala Arg
165 170 175

Gln Leu Ala Glu Ala Val Lys Glu Phe Lys
180 185

<210> 2785
<211> 1227
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1204)
<223> RXA02546

<400> 2785
gattatgtcg gctccaccat cgtggtcagc tacaccgaaa aaccaaacgc ccagggcgca 60

attcagggca attccagttt ctctaggatc gagaaataac atg cca ttg ttt atc 115
Met Pro Leu Phe Ile
1 5

gac gac gcc ctc cac cgc agc aaa aaa tac ttc cac gcg cac tta agc 163
Asp Asp Ala Leu His Arg Ser Lys Lys Tyr Phe His Ala His Leu Ser
10 15 20

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gag ctg ctc ctc ggc gaa ttt gca ggc ctc agc ctg ccc ctg cac cca   211
Glu Leu Leu Leu Gly Glu Phe Ala Gly Leu Ser Leu Pro Leu His Pro
             25                  30                  35

ccg acg gca gct aaa gcc gcc gcc gat att gat gcc acg agg gaa ttt   259
Pro Thr Ala Ala Lys Ala Ala Ala Asp Ile Asp Ala Thr Arg Glu Phe
         40                  45                  50

atc cgc caa tgg gag ggg cgt gat gat gtg gaa tat gcc att cga aac   307
Ile Arg Gln Trp Glu Gly Arg Asp Asp Val Glu Tyr Ala Ile Arg Asn
     55                  60                  65

tgg tct cct gtg ggc tta ggt aaa act gaa gta ccc gtt agg ctg acg   355
Trp Ser Pro Val Gly Leu Gly Lys Thr Glu Val Pro Val Arg Leu Thr
 70                  75                  80                  85

ttg aac acg act gag gaa tta gtt gtg ttt gcg cag gta gag gat gaa   403
Leu Asn Thr Thr Glu Glu Leu Val Val Phe Ala Gln Val Glu Asp Glu
                 90                  95                 100

tgg tct tca ctt cac gag agg ttt tca cag ctg tct ggt ttt aca gcg   451
Trp Ser Ser Leu His Glu Arg Phe Ser Gln Leu Ser Gly Phe Thr Ala
            105                 110                 115

gag gtg gtg gcg aaa cat gtg tcg ctg tgg cgt tcg ctg tct aac gat   499
Glu Val Val Ala Lys His Val Ser Leu Trp Arg Ser Leu Ser Asn Asp
        120                 125                 130

gat ctc tct aag gca gtg tta gtt gtg gat tgg ttt ttg aaa cac cct   547
Asp Leu Ser Lys Ala Val Leu Val Val Asp Trp Phe Leu Lys His Pro
    135                 140                 145

aac tct ggc ctg ctg aaa cgc gcc gtc gca gtt gaa ggc gtg cat acc   595
Asn Ser Gly Leu Leu Lys Arg Ala Val Ala Val Glu Gly Val His Thr
150                 155                 160                 165

aaa tgg ctc gaa aac cac cgc gta ctc att gaa acg tta gtg gcc gac   643
Lys Trp Leu Glu Asn His Arg Val Leu Ile Glu Thr Leu Val Ala Asp
                170                 175                 180

aaa cgt ggt gaa cct ggt cgt gcc gat ctt gga ctt ggt gac gcc gaa   691
Lys Arg Gly Glu Pro Gly Arg Ala Asp Leu Gly Leu Gly Asp Ala Glu
            185                 190                 195

gct cgc gtc cgg ctc cgc ttc cat tcc gta gat gct ccc gct ggg ctc   739
Ala Arg Val Arg Leu Arg Phe His Ser Val Asp Ala Pro Ala Gly Leu
        200                 205                 210

aca gac att gaa gta ccg ctt tcc aac ctg tgt gaa tta caa gaa ccg   787
Thr Asp Ile Glu Val Pro Leu Ser Asn Leu Cys Glu Leu Gln Glu Pro
    215                 220                 225

caa gta att ctg atg gtg gaa aac ctc gat tca ttt ctc gct tta ccc   835
Gln Val Ile Leu Met Val Glu Asn Leu Asp Ser Phe Leu Ala Leu Pro
230                 235                 240                 245

act tgg ccg ggc gta aca att gct tgg ggt gcg ggc tac cgt gca gta   883
Thr Trp Pro Gly Val Thr Ile Ala Trp Gly Ala Gly Tyr Arg Ala Val
                250                 255                 260
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gac att gtt cga gga ccc tac ttt tct aat ggt cgg ttg ctg tac tgg   931
Asp Ile Val Arg Gly Pro Tyr Phe Ser Asn Gly Arg Leu Leu Tyr Trp
            265                 270                 275

ggt gac ctt gac ctg gac ggt ttc aaa att ctc gac ggc gtc cgc agc   979
Gly Asp Leu Asp Leu Asp Gly Phe Lys Ile Leu Asp Gly Val Arg Ser
        280                 285                 290

cat gtt cct cac acc gaa tcc gtg ctg atg aac tct gaa acc gtc tcc   1027
His Val Pro His Thr Glu Ser Val Leu Met Asn Ser Glu Thr Val Ser
    295                 300                 305

cgc tgg cgc tac ctt ggc gtt gcc gac cga gaa ttc aag gca gag agc   1075
Arg Trp Arg Tyr Leu Gly Val Ala Asp Arg Glu Phe Lys Ala Glu Ser
310                 315                 320                 325

ttt gac aac ctt cat gat ttt gaa tct gac gca ctt gac cta ctc att   1123
Phe Asp Asn Leu His Asp Phe Glu Ser Asp Ala Leu Asp Leu Leu Ile
                330                 335                 340

aca gac ggt gag ctc cgc att gaa caa gaa cgc atc cgc ctc gat gtt   1171
Thr Asp Gly Glu Leu Arg Ile Glu Gln Glu Arg Ile Arg Leu Asp Val
            345                 350                 355

gct gtt gaa gaa atc gag aaa gta att cgt ggg tgaagttgtt tcagagttgt 1224
Ala Val Glu Glu Ile Glu Lys Val Ile Arg Gly
        360                 365

ttt                                                               1227


<210> 2786
<211> 368
<212> PRT
<213> Corynebacterium glutamicum

<400> 2786
Met Pro Leu Phe Ile Asp Asp Ala Leu His Arg Ser Lys Lys Tyr Phe
  1               5                  10                  15

His Ala His Leu Ser Glu Leu Leu Leu Gly Glu Phe Ala Gly Leu Ser
             20                  25                  30

Leu Pro Leu His Pro Pro Thr Ala Ala Lys Ala Ala Ala Asp Ile Asp
         35                  40                  45

Ala Thr Arg Glu Phe Ile Arg Gln Trp Glu Gly Arg Asp Asp Val Glu
     50                  55                  60

Tyr Ala Ile Arg Asn Trp Ser Pro Val Gly Leu Gly Lys Thr Glu Val
 65                  70                  75                  80

Pro Val Arg Leu Thr Leu Asn Thr Thr Glu Glu Leu Val Val Phe Ala
                 85                  90                  95

Gln Val Glu Asp Glu Trp Ser Ser Leu His Glu Arg Phe Ser Gln Leu
            100                 105                 110

Ser Gly Phe Thr Ala Glu Val Val Ala Lys His Val Ser Leu Trp Arg
        115                 120                 125
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Ser Leu Ser Asn Asp Asp Leu Ser Lys Ala Val Leu Val Val Asp Trp
    130                 135                 140

Phe Leu Lys His Pro Asn Ser Gly Leu Leu Lys Arg Ala Val Ala Val
145                 150                 155                 160

Glu Gly Val His Thr Lys Trp Leu Glu Asn His Arg Val Leu Ile Glu
                165                 170                 175

Thr Leu Val Ala Asp Lys Arg Gly Glu Pro Gly Arg Ala Asp Leu Gly
            180                 185                 190

Leu Gly Asp Ala Glu Ala Arg Val Arg Leu Arg Phe His Ser Val Asp
        195                 200                 205

Ala Pro Ala Gly Leu Thr Asp Ile Glu Val Pro Leu Ser Asn Leu Cys
    210                 215                 220

Glu Leu Gln Glu Pro Gln Val Ile Leu Met Val Glu Asn Leu Asp Ser
225                 230                 235                 240

Phe Leu Ala Leu Pro Thr Trp Pro Gly Val Thr Ile Ala Trp Gly Ala
                245                 250                 255

Gly Tyr Arg Ala Val Asp Ile Val Arg Gly Pro Tyr Phe Ser Asn Gly
            260                 265                 270

Arg Leu Leu Tyr Trp Gly Asp Leu Asp Leu Asp Gly Phe Lys Ile Leu
        275                 280                 285

Asp Gly Val Arg Ser His Val Pro His Thr Glu Ser Val Leu Met Asn
    290                 295                 300

Ser Glu Thr Val Ser Arg Trp Arg Tyr Leu Gly Val Ala Asp Arg Glu
305                 310                 315                 320

Phe Lys Ala Glu Ser Phe Asp Asn Leu His Asp Phe Glu Ser Asp Ala
                325                 330                 335

Leu Asp Leu Leu Ile Thr Asp Gly Glu Leu Arg Ile Glu Gln Glu Arg
            340                 345                 350

Ile Arg Leu Asp Val Ala Val Glu Glu Ile Glu Lys Val Ile Arg Gly
        355                 360                 365
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<210> 2787
<211> 1326
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1326)
<223> RXA02549

<400> 2787
acc ctc act gca atc tcc tcc gaa act tgg cct atc atg ctc gcg cca 48

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Thr Leu Thr Ala Ile Ser Ser Glu Thr Trp Pro Ile Met Leu Ala Pro
  1               5                  10                  15

tgg gta tgt ctg cct ctg ctt tcg cga aat gtg gat gca cgg gcc atc   96
Trp Val Cys Leu Pro Leu Leu Ser Arg Asn Val Asp Ala Arg Ala Ile
             20                  25                  30

gcg ttg tcc tta ctt ccc gcg gca tgc atg ggt gca gtt aat gcc acc   144
Ala Leu Ser Leu Leu Pro Ala Ala Cys Met Gly Ala Val Asn Ala Thr
         35                  40                  45

gcc acg atg gca gca ctc atc ccg gca gcg ctg atc ttg ctg tat aga   192
Ala Thr Met Ala Ala Leu Ile Pro Ala Ala Leu Ile Leu Leu Tyr Arg
     50                  55                  60

ggg ctc ttc tta agg ctg ctt ctg tgg gga atg ggc gtt ctc gct gtt   240
Gly Leu Phe Leu Arg Leu Leu Leu Trp Gly Met Gly Val Leu Ala Val
 65                  70                  75                  80

aat tca tgg tgg atc gga cct ttg ttg gtg ctt ggc aaa tac gcc ccg   288
Asn Ser Trp Trp Ile Gly Pro Leu Leu Val Leu Gly Lys Tyr Ala Pro
                 85                  90                  95

ccc ttc acc gaa ttc atc gaa agt tcc tcc gtc acc act tcc tgg ctc   336
Pro Phe Thr Glu Phe Ile Glu Ser Ser Ser Val Thr Thr Ser Trp Leu
            100                 105                 110

aac cca gta gaa ata ctc cgc gga acc acc agt tgg aca ccc ttc gta   384
Asn Pro Val Glu Ile Leu Arg Gly Thr Thr Ser Trp Thr Pro Phe Val
        115                 120                 125

gac act gaa cga caa gcc gga tat ctc ctg gtc aac gat gct ctc ttt   432
Asp Thr Glu Arg Gln Ala Gly Tyr Leu Leu Val Asn Asp Ala Leu Phe
    130                 135                 140

gtc acc ctc agc gtt ctc gtc gca gcc ctc ggc ttg atc ggc ctc acc   480
Val Thr Leu Ser Val Leu Val Ala Ala Leu Gly Leu Ile Gly Leu Thr
145                 150                 155                 160

ttg atg aaa cac cgt gga ctg tgg gca ttc atg ctg gcc atc gga ctc   528
Leu Met Lys His Arg Gly Leu Trp Ala Phe Met Leu Ala Ile Gly Leu
                165                 170                 175

ctc atc ctc ggc agc gcc cac cta acg gct gtt caa gaa ttc ctc gac   576
Leu Ile Leu Gly Ser Ala His Leu Thr Ala Val Gln Glu Phe Leu Asp
            180                 185                 190

ggc cca ggc gca gca ctt cga aac atc cac aaa ttt gat cta tta gtc   624
Gly Pro Gly Ala Ala Leu Arg Asn Ile His Lys Phe Asp Leu Leu Val
        195                 200                 205

cgc atg ccg ttg atg gtg ggc gtt gcc gca ttg ggg tcg cat atc agt   672
Arg Met Pro Leu Met Val Gly Val Ala Ala Leu Gly Ser His Ile Ser
    210                 215                 220

ctg ccc ttg ctt ggg acg act gca ttg acc agc gga caa ggc aaa cac   720
Leu Pro Leu Leu Gly Thr Thr Ala Leu Thr Ser Gly Gln Gly Lys His
225                 230                 235                 240

cac acc atc ccg ctg cct ctc caa aaa cgc caa gcc gca gga ctc ctc   768
His Thr Ile Pro Leu Pro Leu Gln Lys Arg Gln Ala Ala Gly Leu Leu
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                245                 250                 255

gtg gtg atc atc gct gtc ggt gct ctt gct ccc gca tgg tcg gca cgg   816
Val Val Ile Ile Ala Val Gly Ala Leu Ala Pro Ala Trp Ser Ala Arg
            260                 265                 270

ctg cta cct cag gga acg tgg gat gaa gtg cct gac tac tgg tac gaa   864
Leu Leu Pro Gln Gly Thr Trp Asp Glu Val Pro Asp Tyr Trp Tyr Glu
        275                 280                 285

gcc aca gaa ttc ctc aac caa aac gcc aca ggc acc cgc acg ttg att   912
Ala Thr Glu Phe Leu Asn Gln Asn Ala Thr Gly Thr Arg Thr Leu Ile
    290                 295                 300

tgg cct agc tcg ccg ttt gcc cgc cag gac tgg gga tgg act cgg gat   960
Trp Pro Ser Ser Pro Phe Ala Arg Gln Asp Trp Gly Trp Thr Arg Asp
305                 310                 315                 320

gaa cca gct caa cca ctt ctt gat gtt ccg tgg gct gtc cgc gat gcc   1008
Glu Pro Ala Gln Pro Leu Leu Asp Val Pro Trp Ala Val Arg Asp Ala
                325                 330                 335

att cct ttg gtt ccc ccg gag gcg att cgc gga tta gat ggt ctc gac   1056
Ile Pro Leu Val Pro Pro Glu Ala Ile Arg Gly Leu Asp Gly Leu Asp
            340                 345                 350

gac cta ggc act cta ggc acc ggt cta aac gac gag gct tta aaa cgt   1104
Asp Leu Gly Thr Leu Gly Thr Gly Leu Asn Asp Glu Ala Leu Lys Arg
        355                 360                 365

cta ggc atc ggc gca gta ctg gtg agg cat gat ctg gaa gcc gac cca   1152
Leu Gly Ile Gly Ala Val Leu Val Arg His Asp Leu Glu Ala Asp Pro
    370                 375                 380

gat att gag gtg gat ctg cct ggg gaa aag cac act ttt ggc tcc caa   1200
Asp Ile Glu Val Asp Leu Pro Gly Glu Lys His Thr Phe Gly Ser Gln
385                 390                 395                 400

ggc caa gta gac gtc tac ctc acc gac ccc gac cgc aat atg tgg atc   1248
Gly Gln Val Asp Val Tyr Leu Thr Asp Pro Asp Arg Asn Met Trp Ile
                405                 410                 415

act tcc ggc aca tcc aag cag ctg ccc acc gtc gct ggc ggc ggc gaa   1296
Thr Ser Gly Thr Ser Lys Gln Leu Pro Thr Val Ala Gly Gly Gly Glu
            420                 425                 430

atc ctc tcg ctc cta gac acc atc aac ggc                          1326
Ile Leu Ser Leu Leu Asp Thr Ile Asn Gly
        435                 440
```

<210> 2788
<211> 442
<212> PRT
<213> Corynebacterium glutamicum

<400> 2788

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Thr Leu Thr Ala Ile Ser Ser Glu Thr Trp Pro Ile Met Leu Ala Pro
  1               5                  10                  15

Trp Val Cys Leu Pro Leu Leu Ser Arg Asn Val Asp Ala Arg Ala Ile
```

```
                20                  25                  30

Ala Leu Ser Leu Leu Pro Ala Ala Cys Met Gly Ala Val Asn Ala Thr
         35                  40                  45

Ala Thr Met Ala Ala Leu Ile Pro Ala Ala Leu Ile Leu Leu Tyr Arg
     50                  55                  60

Gly Leu Phe Leu Arg Leu Leu Leu Trp Gly Met Gly Val Leu Ala Val
 65                  70                  75                  80

Asn Ser Trp Trp Ile Gly Pro Leu Leu Val Leu Gly Lys Tyr Ala Pro
                85                  90                  95

Pro Phe Thr Glu Phe Ile Glu Ser Ser Ser Val Thr Thr Ser Trp Leu
            100                 105                 110

Asn Pro Val Glu Ile Leu Arg Gly Thr Thr Ser Trp Thr Pro Phe Val
        115                 120                 125

Asp Thr Glu Arg Gln Ala Gly Tyr Leu Leu Val Asn Asp Ala Leu Phe
    130                 135                 140

Val Thr Leu Ser Val Leu Val Ala Ala Leu Gly Leu Ile Gly Leu Thr
145                 150                 155                 160

Leu Met Lys His Arg Gly Leu Trp Ala Phe Met Leu Ala Ile Gly Leu
                165                 170                 175

Leu Ile Leu Gly Ser Ala His Leu Thr Ala Val Gln Glu Phe Leu Asp
            180                 185                 190

Gly Pro Gly Ala Ala Leu Arg Asn Ile His Lys Phe Asp Leu Leu Val
        195                 200                 205

Arg Met Pro Leu Met Val Gly Val Ala Ala Leu Gly Ser His Ile Ser
    210                 215                 220

Leu Pro Leu Leu Gly Thr Thr Ala Leu Thr Ser Gly Gln Gly Lys His
225                 230                 235                 240

His Thr Ile Pro Leu Pro Leu Gln Lys Arg Gln Ala Ala Gly Leu Leu
                245                 250                 255

Val Val Ile Ile Ala Val Gly Ala Leu Ala Pro Ala Trp Ser Ala Arg
            260                 265                 270

Leu Leu Pro Gln Gly Thr Trp Asp Glu Val Pro Asp Tyr Trp Tyr Glu
        275                 280                 285

Ala Thr Glu Phe Leu Asn Gln Asn Ala Thr Gly Thr Arg Thr Leu Ile
    290                 295                 300

Trp Pro Ser Ser Pro Phe Ala Arg Gln Asp Trp Gly Trp Thr Arg Asp
305                 310                 315                 320

Glu Pro Ala Gln Pro Leu Leu Asp Val Pro Trp Ala Val Arg Asp Ala
                325                 330                 335

Ile Pro Leu Val Pro Pro Glu Ala Ile Arg Gly Leu Asp Gly Leu Asp
            340                 345                 350
```

```
Asp Leu Gly Thr Leu Gly Thr Gly Leu Asn Asp Glu Ala Leu Lys Arg
        355                 360                 365

Leu Gly Ile Gly Ala Val Leu Val Arg His Asp Leu Glu Ala Asp Pro
    370                 375                 380

Asp Ile Glu Val Asp Leu Pro Gly Glu Lys His Thr Phe Gly Ser Gln
385                 390                 395                 400

Gly Gln Val Asp Val Tyr Leu Thr Asp Pro Asp Arg Asn Met Trp Ile
                405                 410                 415

Thr Ser Gly Thr Ser Lys Gln Leu Pro Thr Val Ala Gly Gly Gly Glu
            420                 425                 430

Ile Leu Ser Leu Leu Asp Thr Ile Asn Gly
        435                 440


<210> 2789
<211> 918
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(895)
<223> RXA02552

<400> 2789
tccttaaata cccactgtcc tctattctgg gttaggcttc actgggtaaa agtgcctgcc 60

tatgcctgaa acttgagcat ggcaacagca aggagacacc gtg gga aaa cat gca   115
                                              Val Gly Lys His Ala
                                                1               5

gct gaa aca tcg gaa ccg aag aaa aat tca ccg tgg cgc att ggt ttg   163
Ala Glu Thr Ser Glu Pro Lys Lys Asn Ser Pro Trp Arg Ile Gly Leu
                10                  15                  20

ttg acg ttt ttg att tct tca gtt gtc gtg acg ctg gtg ggc atg gtg   211
Leu Thr Phe Leu Ile Ser Ser Val Val Val Thr Leu Val Gly Met Val
            25                  30                  35

atg ctg tgg ccg gat tct gat gat gtg gtg ttg gcg gat aac ttt tcg   259
Met Leu Trp Pro Asp Ser Asp Asp Val Val Leu Ala Asp Asn Phe Ser
        40                  45                  50

cag acg ttt gcg gga aat cat gag cag gtg gat gga acg atc acg ctc   307
Gln Thr Phe Ala Gly Asn His Glu Gln Val Asp Gly Thr Ile Thr Leu
    55                  60                  65

gtt gat aat tct gcg tgt aat tcg cca gac acc ggc cga gtt ttt gcg   355
Val Asp Asn Ser Ala Cys Asn Ser Pro Asp Thr Gly Arg Val Phe Ala
70                  75                  80                  85

gaa agc ccc acg att tct gcg gag ccg gca acg ttg gag tgc gtg cgt   403
Glu Ser Pro Thr Ile Ser Ala Glu Pro Ala Thr Leu Glu Cys Val Arg
                90                  95                  100
```

```
gca ctc gta gac atc aca tcg ggt gcc aat gag ggg cag aaa act cag   451
Ala Leu Val Asp Ile Thr Ser Gly Ala Asn Glu Gly Gln Lys Thr Gln
            105                 110                 115

ctg atc act tac gcg caa cct ggt gat ccg gag ttt tcc gag ggc gac   499
Leu Ile Thr Tyr Ala Gln Pro Gly Asp Pro Glu Phe Ser Glu Gly Asp
        120                 125                 130

aag atc cgc atg gtg gaa aca ccg gat aca aat ggc gag atc atc tac   547
Lys Ile Arg Met Val Glu Thr Pro Asp Thr Asn Gly Glu Ile Ile Tyr
    135                 140                 145

acc ttt gct gat tac cag cgc gga ccg gcg ttg atc att tgg ggt gtg   595
Thr Phe Ala Asp Tyr Gln Arg Gly Pro Ala Leu Ile Ile Trp Gly Val
150                 155                 160                 165

gtt ctc att gtg gcg atg gga gct ttc gcg gcg tgg cga ggt gtg cgt   643
Val Leu Ile Val Ala Met Gly Ala Phe Ala Ala Trp Arg Gly Val Arg
                170                 175                 180

gcg ctg gtt ggt ttg gtc gtc acc ttg gga att gtt ggt att ttc ttg   691
Ala Leu Val Gly Leu Val Val Thr Leu Gly Ile Val Gly Ile Phe Leu
            185                 190                 195

ctg cca gga ttg gcc agc ggg cac gat gcg atg tgg ttg gcg ctg gtg   739
Leu Pro Gly Leu Ala Ser Gly His Asp Ala Met Trp Leu Ala Leu Val
        200                 205                 210

tgt ggc gcg gcg atc ttg ttg att gtg gtg ccg atg gtt cac gga atc   787
Cys Gly Ala Ala Ile Leu Leu Ile Val Val Pro Met Val His Gly Ile
    215                 220                 225

aac tgg aaa tcg gca gct gcg ttg gcg ggc acg ctg gtg gca ttg ttg   835
Asn Trp Lys Ser Ala Ala Ala Leu Ala Gly Thr Leu Val Ala Leu Leu
230                 235                 240                 245

ttg tcg gcg gtg ttg tcg tgg gcg tcg atc gtc acc act gaa ttt gcg   883
Leu Ser Ala Val Leu Ser Trp Ala Ser Ile Val Thr Thr Glu Phe Ala
                250                 255                 260

cgg act ggg cga tgagaatcat ctgaagatca tca                        918
Arg Thr Gly Arg
            265
```

<210> 2790
<211> 265
<212> PRT
<213> Corynebacterium glutamicum

<400> 2790

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Val Gly Lys His Ala Ala Glu Thr Ser Glu Pro Lys Lys Asn Ser Pro
  1               5                  10                  15

Trp Arg Ile Gly Leu Leu Thr Phe Leu Ile Ser Ser Val Val Val Thr
             20                  25                  30

Leu Val Gly Met Val Met Leu Trp Pro Asp Ser Asp Asp Val Val Leu
         35                  40                  45

Ala Asp Asn Phe Ser Gln Thr Phe Ala Gly Asn His Glu Gln Val Asp
```

```
     50                  55                  60

Gly Thr Ile Thr Leu Val Asp Asn Ser Ala Cys Asn Ser Pro Asp Thr
 65                  70                  75                  80

Gly Arg Val Phe Ala Glu Ser Pro Thr Ile Ser Ala Glu Pro Ala Thr
                85                  90                  95

Leu Glu Cys Val Arg Ala Leu Val Asp Ile Thr Ser Gly Ala Asn Glu
            100                 105                 110

Gly Gln Lys Thr Gln Leu Ile Thr Tyr Ala Gln Pro Gly Asp Pro Glu
        115                 120                 125

Phe Ser Glu Gly Asp Lys Ile Arg Met Val Glu Thr Pro Asp Thr Asn
    130                 135                 140

Gly Glu Ile Ile Tyr Thr Phe Ala Asp Tyr Gln Arg Gly Pro Ala Leu
145                 150                 155                 160

Ile Ile Trp Gly Val Val Leu Ile Val Ala Met Gly Ala Phe Ala Ala
                165                 170                 175

Trp Arg Gly Val Arg Ala Leu Val Gly Leu Val Val Thr Leu Gly Ile
            180                 185                 190

Val Gly Ile Phe Leu Leu Pro Gly Leu Ala Ser Gly His Asp Ala Met
        195                 200                 205

Trp Leu Ala Leu Val Cys Gly Ala Ala Ile Leu Leu Ile Val Val Pro
    210                 215                 220

Met Val His Gly Ile Asn Trp Lys Ser Ala Ala Ala Leu Ala Gly Thr
225                 230                 235                 240

Leu Val Ala Leu Leu Leu Ser Ala Val Leu Ser Trp Ala Ser Ile Val
                245                 250                 255

Thr Thr Glu Phe Ala Arg Thr Gly Arg
            260                 265


<210> 2791
<211> 747
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(724)
<223> RXA02554

<400> 2791
gcttttgaag tgtgtcgcgt gtgcggactg aaatagtttc cgcttcaact tggttgctaa 60

ggataggctc cataaaaata accaaaggcg gaaaatttca atg tca cac act aag   115
                                               Met Ser His Thr Lys
                                                 1               5

cca tcc att gcc atc ctc ggt gct ggc cga gtg ggt tct tca ctt gcc   163
Pro Ser Ile Ala Ile Leu Gly Ala Gly Arg Val Gly Ser Ser Leu Ala
```

```
                  10                  15                  20

agg tca gcg gtc gcc gca ggc tat gag gta aag gtt gct ggt tca ggt   211
Arg Ser Ala Val Ala Ala Gly Tyr Glu Val Lys Val Ala Gly Ser Gly
             25                  30                  35

gct gtg gac aaa atc gct ctt acc gct gag atc ctt atg ccc ggc gcg   259
Ala Val Asp Lys Ile Ala Leu Thr Ala Glu Ile Leu Met Pro Gly Ala
         40                  45                  50

gtt cca agc act gct gac cag gct gta aag gat gca gat att gtg ttc   307
Val Pro Ser Thr Ala Asp Gln Ala Val Lys Asp Ala Asp Ile Val Phe
     55                  60                  65

ttg gct gtt ccc ctg cat aaa ttc cgc agt gtc aat cca gcc act tta   355
Leu Ala Val Pro Leu His Lys Phe Arg Ser Val Asn Pro Ala Thr Leu
 70                  75                  80                  85

gag ggc aag atc gtt att gac acg atg aac cac tgg gtt ccg gtc aat   403
Glu Gly Lys Ile Val Ile Asp Thr Met Asn His Trp Val Pro Val Asn
                 90                  95                 100

ggt gag ttg gag gaa att gat cag gat ccg cgc agc act tcg gag att   451
Gly Glu Leu Glu Glu Ile Asp Gln Asp Pro Arg Ser Thr Ser Glu Ile
            105                 110                 115

att gcg gag ttt ttc gcg gga tca acc atg gtg aag tct ttt aac cac   499
Ile Ala Glu Phe Phe Ala Gly Ser Thr Met Val Lys Ser Phe Asn His
        120                 125                 130

att ggt tat cac gag att gag cag gat gcg ggt acc ggg cgt gcg att   547
Ile Gly Tyr His Glu Ile Glu Gln Asp Ala Gly Thr Gly Arg Ala Ile
    135                 140                 145

gcg tat gcc acg gat gat gtg gat gca ggt gcc cag gtt gca cag cta   595
Ala Tyr Ala Thr Asp Asp Val Asp Ala Gly Ala Gln Val Ala Gln Leu
150                 155                 160                 165

att aag agt ttt ggg ttt gtt cct tta aat att ggc gca ttg gaa aac   643
Ile Lys Ser Phe Gly Phe Val Pro Leu Asn Ile Gly Ala Leu Glu Asn
                170                 175                 180

ggc cgt att ctg gaa cct ggc caa gaa gct ttc ggc gcg cac ctt aat   691
Gly Arg Ile Leu Glu Pro Gly Gln Glu Ala Phe Gly Ala His Leu Asn
            185                 190                 195

aaa gat tcg cgc cta gaa ctt gtt aat cag cgg tagtacctcg atcttcagcc 744
Lys Asp Ser Arg Leu Glu Leu Val Asn Gln Arg
        200                 205

aac                                                               747
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<210> 2792
<211> 208
<212> PRT
<213> Corynebacterium glutamicum

<400> 2792

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Met Ser His Thr Lys Pro Ser Ile Ala Ile Leu Gly Ala Gly Arg Val
  1               5                  10                  15
```

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Gly Ser Ser Leu Ala Arg Ser Ala Val Ala Ala Gly Tyr Glu Val Lys
            20                  25                  30

Val Ala Gly Ser Gly Ala Val Asp Lys Ile Ala Leu Thr Ala Glu Ile
        35                  40                  45

Leu Met Pro Gly Ala Val Pro Ser Thr Ala Asp Gln Ala Val Lys Asp
    50                  55                  60

Ala Asp Ile Val Phe Leu Ala Val Pro Leu His Lys Phe Arg Ser Val
65                  70                  75                  80

Asn Pro Ala Thr Leu Glu Gly Lys Ile Val Ile Asp Thr Met Asn His
                85                  90                  95

Trp Val Pro Val Asn Gly Glu Leu Glu Glu Ile Asp Gln Asp Pro Arg
            100                 105                 110

Ser Thr Ser Glu Ile Ile Ala Glu Phe Phe Ala Gly Ser Thr Met Val
        115                 120                 125

Lys Ser Phe Asn His Ile Gly Tyr His Glu Ile Glu Gln Asp Ala Gly
    130                 135                 140

Thr Gly Arg Ala Ile Ala Tyr Ala Thr Asp Asp Val Asp Ala Gly Ala
145                 150                 155                 160

Gln Val Ala Gln Leu Ile Lys Ser Phe Gly Phe Val Pro Leu Asn Ile
                165                 170                 175

Gly Ala Leu Glu Asn Gly Arg Ile Leu Glu Pro Gly Gln Glu Ala Phe
            180                 185                 190

Gly Ala His Leu Asn Lys Asp Ser Arg Leu Glu Leu Val Asn Gln Arg
        195                 200                 205
```

<210> 2793
<211> 854
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (82)..(831)
<223> RXA02569

<400> 2793
aatcttcaaa tcgttcccgc aagcaaaagg tgacatactg ctggcttgtt tttgcattcg 60

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acgatctgca tggggattac tatg tca cgc tca tct aaa att tcg gtc gcg    111
                       Met Ser Arg Ser Ser Lys Ile Ser Val Ala
                         1               5                  10

ttt ggt ggc cta ctc atc gct gct acc tgg ctg tat ttg gtc ttg gtc   159
Phe Gly Gly Leu Leu Ile Ala Ala Thr Trp Leu Tyr Leu Val Leu Val
                15                  20                  25
```

```
agg cct acc gat tgg gaa tca gtg ggt ggt tcc acg gaa gcg ttg atc   207
Arg Pro Thr Asp Trp Glu Ser Val Gly Gly Ser Thr Glu Ala Leu Ile
            30                  35                  40

acg ttg gtg ggc tat gtt gcc ggc acg atc gcg ttg ttg gtt ggt gtg   255
Thr Leu Val Gly Tyr Val Ala Gly Thr Ile Ala Leu Leu Val Gly Val
        45                  50                  55

ctg cct acg ctt cca gcc agg acc att gcg atc att cct gtg gct ttg   303
Leu Pro Thr Leu Pro Ala Arg Thr Ile Ala Ile Ile Pro Val Ala Leu
    60                  65                  70

gtg ctc aat att ttg tta ggc caa gtc act ggt tct ttt gtc att ccg   351
Val Leu Asn Ile Leu Leu Gly Gln Val Thr Gly Ser Phe Val Ile Pro
75                  80                  85                  90

ctg tat tta gat gcg gtg ggc aca gtg ctg gtc gca gct ctt gct ggt   399
Leu Tyr Leu Asp Ala Val Gly Thr Val Leu Val Ala Ala Leu Ala Gly
                95                  100                 105

cct agt gct ggt ttg gca aca ggt gct tta agt tct gtg gtg tgg gcg   447
Pro Ser Ala Gly Leu Ala Thr Gly Ala Leu Ser Ser Val Val Trp Ala
            110                 115                 120

ttg ttc aat ccg ctg gct ttg ccg ttt gct gca ggt tcc gcg ctg act   495
Leu Phe Asn Pro Leu Ala Leu Pro Phe Ala Ala Gly Ser Ala Leu Thr
        125                 130                 135

ggt tgg ttg acc ggt gtg gtg att aaa aag ggt gcg ttt aag aat atc   543
Gly Trp Leu Thr Gly Val Val Ile Lys Lys Gly Ala Phe Lys Asn Ile
    140                 145                 150

ttc gcc acc atc atc tct ggt gcg gtc att ggt ttg atc acg ggt gct   591
Phe Ala Thr Ile Ile Ser Gly Ala Val Ile Gly Leu Ile Thr Gly Ala
155                 160                 165                 170

gtc gct gcc ccg gtt gcg gcg ttt gtt tat ggc gga acc gcc ggt gtg   639
Val Ala Ala Pro Val Ala Ala Phe Val Tyr Gly Gly Thr Ala Gly Val
                175                 180                 185

gga act ggt gcg gtg gtt agc ctc ttc cgc gaa atg ggt aac tct ttg   687
Gly Thr Gly Ala Val Val Ser Leu Phe Arg Glu Met Gly Asn Ser Leu
            190                 195                 200

ctc gca tcg gta acc tgg cag tcg ttt att tcc gat cct ttg gat aag   735
Leu Ala Ser Val Thr Trp Gln Ser Phe Ile Ser Asp Pro Leu Asp Lys
        205                 210                 215

gcc att gtt atg ctc att gtg ttt gtg gtg gtc aag tcg cta ccc aag   783
Ala Ile Val Met Leu Ile Val Phe Val Val Val Lys Ser Leu Pro Lys
    220                 225                 230

cgc acc act agg gca ttg gtt ccg cag cgg gtt ccg gag gac gtc gct   831
Arg Thr Thr Arg Ala Leu Val Pro Gln Arg Val Pro Glu Asp Val Ala
235                 240                 245                 250

taaacatgaa tcctttgaca tgg                                        854
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<210> 2794

<211> 250
<212> PRT
<213> Corynebacterium glutamicum

<400> 2794
Met Ser Arg Ser Ser Lys Ile Ser Val Ala Phe Gly Gly Leu Leu Ile
1 5 10 15

Ala Ala Thr Trp Leu Tyr Leu Val Leu Val Arg Pro Thr Asp Trp Glu
20 25 30

Ser Val Gly Gly Ser Thr Glu Ala Leu Ile Thr Leu Val Gly Tyr Val
35 40 45

Ala Gly Thr Ile Ala Leu Leu Val Gly Val Leu Pro Thr Leu Pro Ala
50 55 60

Arg Thr Ile Ala Ile Ile Pro Val Ala Leu Val Leu Asn Ile Leu Leu
65 70 75 80

Gly Gln Val Thr Gly Ser Phe Val Ile Pro Leu Tyr Leu Asp Ala Val
85 90 95

Gly Thr Val Leu Val Ala Ala Leu Ala Gly Pro Ser Ala Gly Leu Ala
100 105 110

Thr Gly Ala Leu Ser Ser Val Val Trp Ala Leu Phe Asn Pro Leu Ala
115 120 125

Leu Pro Phe Ala Ala Gly Ser Ala Leu Thr Gly Trp Leu Thr Gly Val
130 135 140

Val Ile Lys Lys Gly Ala Phe Lys Asn Ile Phe Ala Thr Ile Ile Ser
145 150 155 160

Gly Ala Val Ile Gly Leu Ile Thr Gly Ala Val Ala Ala Pro Val Ala
165 170 175

Ala Phe Val Tyr Gly Gly Thr Ala Gly Val Gly Thr Gly Ala Val Val
180 185 190

Ser Leu Phe Arg Glu Met Gly Asn Ser Leu Leu Ala Ser Val Thr Trp
195 200 205

Gln Ser Phe Ile Ser Asp Pro Leu Asp Lys Ala Ile Val Met Leu Ile
210 215 220

Val Phe Val Val Val Lys Ser Leu Pro Lys Arg Thr Thr Arg Ala Leu
225 230 235 240

Val Pro Gln Arg Val Pro Glu Asp Val Ala
245 250

<210> 2795
<211> 765
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

<222> (101)..(742)
<223> RXA02570

<400> 2795
ccattgttat gctcattgtg tttgtggtgg tcaagtcgct acccaagcgc accactaggg 60

cattggttcc gcagcgggtt ccggaggacg tcgcttaaac atg aat cct ttg aca 115
Met Asn Pro Leu Thr
1 5

tgg atc att ggc gca ttc agc atg tgg atc gtg gtg ctg ggc gtt aat 163
Trp Ile Ile Gly Ala Phe Ser Met Trp Ile Val Val Leu Gly Val Asn
10 15 20

aag ctt ggt tta agc atc gca gtg atc atc atc gcg cag gtc gtg gcg 211
Lys Leu Gly Leu Ser Ile Ala Val Ile Ile Ile Ala Gln Val Val Ala
25 30 35

atg att cgg gtg cgc aat gta tct gtg ttg gct tca aca gca ttg tta 259
Met Ile Arg Val Arg Asn Val Ser Val Leu Ala Ser Thr Ala Leu Leu
40 45 50

tcg gtt cct gca ttg gcc tcg atg gcg ctg att cac atg ccg tat tct 307
Ser Val Pro Ala Leu Ala Ser Met Ala Leu Ile His Met Pro Tyr Ser
55 60 65

tcc gac ggc tgg ttg att gct ctt acc ttg acg gct cgt ttt agt gcg 355
Ser Asp Gly Trp Leu Ile Ala Leu Thr Leu Thr Ala Arg Phe Ser Ala
70 75 80 85

ttg atg tct att ttc ctc ctt gca gca aca gcg att act att cct gag 403
Leu Met Ser Ile Phe Leu Leu Ala Ala Thr Ala Ile Thr Ile Pro Glu
90 95 100

ctg gtg aaa tcc cta tat cgt tgg ccc aag ctg gcg tat atc gtg ggt 451
Leu Val Lys Ser Leu Tyr Arg Trp Pro Lys Leu Ala Tyr Ile Val Gly
105 110 115

tct gca ttg cag atg att ccg cag ggt aaa cag acc ttg gcg ttg gtt 499
Ser Ala Leu Gln Met Ile Pro Gln Gly Lys Gln Thr Leu Ala Leu Val
120 125 130

cgt gat gcc aat gct ttg cgc ggg cgc agc gtt aaa ggt ccc gtg cgc 547
Arg Asp Ala Asn Ala Leu Arg Gly Arg Ser Val Lys Gly Pro Val Arg
135 140 145

gcg gtg aaa tat gtg ggt ttg ccc ctg att aca cat tta ctt agt gca 595
Ala Val Lys Tyr Val Gly Leu Pro Leu Ile Thr His Leu Leu Ser Ala
150 155 160 165

ggt gcc gcg cga gcg att ccc ttg gag gtc gca ggc ctg gac agg ccg 643
Gly Ala Ala Arg Ala Ile Pro Leu Glu Val Ala Gly Leu Asp Arg Pro
170 175 180

ggg ccg cgt acg gtg ttg gtt gag gtg gtg gag ggg cgc gtc gaa aag 691
Gly Pro Arg Thr Val Leu Val Glu Val Val Glu Gly Arg Val Glu Lys
185 190 195

cat tgt cgc tgg ttg ttg ccg ctt ttg gca gtc ggg atg gcg tgg tgg 739
His Cys Arg Trp Leu Leu Pro Leu Leu Ala Val Gly Met Ala Trp Trp
200 205 210

ctc taactcaaat cgtcggaccg tcc 765
Leu

<210> 2796
<211> 214
<212> PRT
<213> Corynebacterium glutamicum

<400> 2796
Met Asn Pro Leu Thr Trp Ile Ile Gly Ala Phe Ser Met Trp Ile Val
1 5 10 15

Val Leu Gly Val Asn Lys Leu Gly Leu Ser Ile Ala Val Ile Ile Ile
20 25 30

Ala Gln Val Val Ala Met Ile Arg Val Arg Asn Val Ser Val Leu Ala
35 40 45

Ser Thr Ala Leu Leu Ser Val Pro Ala Leu Ala Ser Met Ala Leu Ile
50 55 60

His Met Pro Tyr Ser Ser Asp Gly Trp Leu Ile Ala Leu Thr Leu Thr
65 70 75 80

Ala Arg Phe Ser Ala Leu Met Ser Ile Phe Leu Leu Ala Ala Thr Ala
85 90 95

Ile Thr Ile Pro Glu Leu Val Lys Ser Leu Tyr Arg Trp Pro Lys Leu
100 105 110

Ala Tyr Ile Val Gly Ser Ala Leu Gln Met Ile Pro Gln Gly Lys Gln
115 120 125

Thr Leu Ala Leu Val Arg Asp Ala Asn Ala Leu Arg Gly Arg Ser Val
130 135 140

Lys Gly Pro Val Arg Ala Val Lys Tyr Val Gly Leu Pro Leu Ile Thr
145 150 155 160

His Leu Leu Ser Ala Gly Ala Ala Arg Ala Ile Pro Leu Glu Val Ala
165 170 175

Gly Leu Asp Arg Pro Gly Pro Arg Thr Val Leu Val Glu Val Val Glu
180 185 190

Gly Arg Val Glu Lys His Cys Arg Trp Leu Leu Pro Leu Leu Ala Val
195 200 205

Gly Met Ala Trp Trp Leu
210

<210> 2797
<211> 567
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS
<222> (101)..(544)
<223> RXA02573

<400> 2797
cttccacacg gctctaacta taggaaaaga cggcagcaaa gcattaatcg tcggtaggct 60

gaagtgaagt actttccgaa agattcacag ggagcatgca atg acg aac aaa acc 115
Met Thr Asn Lys Thr
1 5

atg ctg gtt gct ttt gat ggc tca ccg gaa tcc cgg cgc gct ttg gaa 163
Met Leu Val Ala Phe Asp Gly Ser Pro Glu Ser Arg Arg Ala Leu Glu
10 15 20

tat gcg gcg aaa ttg ttg cag ccg cgc acc gtg gaa att tta act gcg 211
Tyr Ala Ala Lys Leu Leu Gln Pro Arg Thr Val Glu Ile Leu Thr Ala
25 30 35

tgg gag cca ttg cat cgg caa gct gcg cgc tcg gtt tcg ttg atc acc 259
Trp Glu Pro Leu His Arg Gln Ala Ala Arg Ser Val Ser Leu Ile Thr
40 45 50

ttg ggg gtg gaa ccc gaa gac ccc gcc cat tcc gct gca cta aaa acc 307
Leu Gly Val Glu Pro Glu Asp Pro Ala His Ser Ala Ala Leu Lys Thr
55 60 65

tgc cag gaa ggc gta gag cta gcc caa tct cta ggt ctg gaa gcg cga 355
Cys Gln Glu Gly Val Glu Leu Ala Gln Ser Leu Gly Leu Glu Ala Arg
70 75 80 85

gcc cac atg gtg gaa tcc gca acg gcc gtg tgg agc gcc atc gtt gat 403
Ala His Met Val Glu Ser Ala Thr Ala Val Trp Ser Ala Ile Val Asp
90 95 100

gct gct gac gag ctc cgc ccc gac gtg att gtc acc ggc acc cgc ggg 451
Ala Ala Asp Glu Leu Arg Pro Asp Val Ile Val Thr Gly Thr Arg Gly
105 110 115

atc tcc gga tgg aaa tcc ctg tgg caa tcc tcc acc tca gac agc gtg 499
Ile Ser Gly Trp Lys Ser Leu Trp Gln Ser Ser Thr Ser Asp Ser Val
120 125 130

ctc cac cac gcc gac gta cca gtt ttt gtc gtt cca ccc ctg gac 544
Leu His His Ala Asp Val Pro Val Phe Val Val Pro Pro Leu Asp
135 140 145

taaaaccgag acgagaacca aga 567

<210> 2798
<211> 148
<212> PRT
<213> Corynebacterium glutamicum

<400> 2798
Met Thr Asn Lys Thr Met Leu Val Ala Phe Asp Gly Ser Pro Glu Ser
1 5 10 15

Arg Arg Ala Leu Glu Tyr Ala Ala Lys Leu Leu Gln Pro Arg Thr Val
20 25 30

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Glu Ile Leu Thr Ala Trp Glu Pro Leu His Arg Gln Ala Ala Arg Ser
         35                  40                  45

Val Ser Leu Ile Thr Leu Gly Val Glu Pro Glu Asp Pro Ala His Ser
     50                  55                  60

Ala Ala Leu Lys Thr Cys Gln Glu Gly Val Glu Leu Ala Gln Ser Leu
 65                  70                  75                  80

Gly Leu Glu Ala Arg Ala His Met Val Glu Ser Ala Thr Ala Val Trp
                85                  90                  95

Ser Ala Ile Val Asp Ala Ala Asp Glu Leu Arg Pro Asp Val Ile Val
            100                 105                 110

Thr Gly Thr Arg Gly Ile Ser Gly Trp Lys Ser Leu Trp Gln Ser Ser
        115                 120                 125

Thr Ser Asp Ser Val Leu His His Ala Asp Val Pro Val Phe Val Val
    130                 135                 140

Pro Pro Leu Asp
145
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<210> 2799
<211> 1258
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(1258)
<223> RXA02575

<400> 2799

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tgagtaggaa tttcgcatca gtgcaactag cctttcaggt gtg aag aac tct ggg   115
                                            Val Lys Asn Ser Gly
                                              1               5

aaa aat tcg gca aag aat cgg acc aaa ggg atc cta atc ggg gtt ctc   163
Lys Asn Ser Ala Lys Asn Arg Thr Lys Gly Ile Leu Ile Gly Val Leu
                 10                  15                  20

gtt ggt ctg att gcc att ttt gca ggc atc tat gcg gtc gat gtt ttc   211
Val Gly Leu Ile Ala Ile Phe Ala Gly Ile Tyr Ala Val Asp Val Phe
             25                  30                  35

ctc aac aag gac aac atc cct cgt gga aca acc gtc ggt ggc gtc agt   259
Leu Asn Lys Asp Asn Ile Pro Arg Gly Thr Thr Val Gly Gly Val Ser
         40                  45                  50

att tcc aac ctc agt gca caa gaa gcc cgc aca aag ttg gaa acc gaa   307
Ile Ser Asn Leu Ser Ala Gln Glu Ala Arg Thr Lys Leu Glu Thr Glu
     55                  60                  65

ctg gcc aat gat gtg gtg cag ccc gtc acc gtg acg gca ggg gag cag   355
Leu Ala Asn Asp Val Val Gln Pro Val Thr Val Thr Ala Gly Glu Gln
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 70                  75                  80                  85

agc acc act ttt gat cca gtt gcc tcc ggc gtc ggc atc gat tgg gac   403
Ser Thr Thr Phe Asp Pro Val Ala Ser Gly Val Gly Ile Asp Trp Asp
                90                  95                 100

gca acc atc gaa ggc acc ggc gag cag tct tgg aac ccc att acc cgc   451
Ala Thr Ile Glu Gly Thr Gly Glu Gln Ser Trp Asn Pro Ile Thr Arg
            105                 110                 115

ttc gtg gcg ctg ttc aaa gaa tcc gaa tct ccc atc gtg agc acc gtc   499
Phe Val Ala Leu Phe Lys Glu Ser Glu Ser Pro Ile Val Ser Thr Val
        120                 125                 130

gat ccc gca gcc ttc ggc ccg acc ctt gat cgc atg gtc ggc gaa ctc   547
Asp Pro Ala Ala Phe Gly Pro Thr Leu Asp Arg Met Val Gly Glu Leu
    135                 140                 145

tat cga gat ccc att tcc gga aac ctg cat atc gac gcc ggc acc ctc   595
Tyr Arg Asp Pro Ile Ser Gly Asn Leu His Ile Asp Ala Gly Thr Leu
150                 155                 160                 165

gtg gtc aac gac acc atc gac gga caa gcc gta gac cgc acc att ttg   643
Val Val Asn Asp Thr Ile Asp Gly Gln Ala Val Asp Arg Thr Ile Leu
                170                 175                 180

gaa caa gca gtc aca gaa aac tgg ctc aac cca gag ggc gta aaa gcc   691
Glu Gln Ala Val Thr Glu Asn Trp Leu Asn Pro Glu Gly Val Lys Ala
            185                 190                 195

gag cca tac gtt gtt ccc gct gcg atc agc caa gac acc atc gat aaa   739
Glu Pro Tyr Val Val Pro Ala Ala Ile Ser Gln Asp Thr Ile Asp Lys
        200                 205                 210

ctt gca gaa ggc gcc gga gct aaa gca gta tct agc cct ttc gtc gtc   787
Leu Ala Glu Gly Ala Gly Ala Lys Ala Val Ser Ser Pro Phe Val Val
    215                 220                 225

cga ggc gat gac gga att gaa ggc acc atc ccc gtc gag cgc atg ggt   835
Arg Gly Asp Asp Gly Ile Glu Gly Thr Ile Pro Val Glu Arg Met Gly
230                 235                 240                 245

gaa gtg gtg agt ttc cca gaa gaa aac ggc acc atc cgc gtc gac atc   883
Glu Val Val Ser Phe Pro Glu Glu Asn Gly Thr Ile Arg Val Asp Ile
                250                 255                 260

aat gca gaa gca gca aca gca atg ctg gcc gaa ggt ctc aaa gaa aca   931
Asn Ala Glu Ala Ala Thr Ala Met Leu Ala Glu Gly Leu Lys Glu Thr
            265                 270                 275

gag atc gag ccc acc aac gct caa atc agt ttc tcc tca ggc tcc cgc   979
Glu Ile Glu Pro Thr Asn Ala Gln Ile Ser Phe Ser Ser Gly Ser Arg
        280                 285                 290

gta gtc acc cca gaa gtc acc gga cac gga atc aac tgg gaa gaa acc  1027
Val Val Thr Pro Glu Val Thr Gly His Gly Ile Asn Trp Glu Glu Thr
    295                 300                 305

ctg gcc gat ctg ccc aac aac ctc acc ggc gat ggc ccc cgc acc atc  1075
Leu Ala Asp Leu Pro Asn Asn Leu Thr Gly Asp Gly Pro Arg Thr Ile
310                 315                 320                 325
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gac gca atc tac gag gac acc cca gca aca ttc acc gcc acc gac gcc   1123
Asp Ala Ile Tyr Glu Asp Thr Pro Ala Thr Phe Thr Ala Thr Asp Ala
                330                 335                 340

caa aac gct acc ttc aat gag gtc atg ggc gag ttc acc acc ggc ggc   1171
Gln Asn Ala Thr Phe Asn Glu Val Met Gly Glu Phe Thr Thr Gly Gly
            345                 350                 355

ttc tct gct gcc tcc gga aca aac atc cgc ctc acc gcg caa atg gtc   1219
Phe Ser Ala Ala Ser Gly Thr Asn Ile Arg Leu Thr Ala Gln Met Val
        360                 365                 370

gac ggc gca gtc gtt tca cct ggc gat aca ttc tcc ctc               1258
Asp Gly Ala Val Val Ser Pro Gly Asp Thr Phe Ser Leu
    375                 380                 385


<210> 2800
<211> 386
<212> PRT
<213> Corynebacterium glutamicum

<400> 2800
Val Lys Asn Ser Gly Lys Asn Ser Ala Lys Asn Arg Thr Lys Gly Ile
  1               5                  10                  15

Leu Ile Gly Val Leu Val Gly Leu Ile Ala Ile Phe Ala Gly Ile Tyr
             20                  25                  30

Ala Val Asp Val Phe Leu Asn Lys Asp Asn Ile Pro Arg Gly Thr Thr
         35                  40                  45

Val Gly Gly Val Ser Ile Ser Asn Leu Ser Ala Gln Glu Ala Arg Thr
     50                  55                  60

Lys Leu Glu Thr Glu Leu Ala Asn Asp Val Val Gln Pro Val Thr Val
 65                  70                  75                  80

Thr Ala Gly Glu Gln Ser Thr Thr Phe Asp Pro Val Ala Ser Gly Val
                 85                  90                  95

Gly Ile Asp Trp Asp Ala Thr Ile Glu Gly Thr Gly Glu Gln Ser Trp
            100                 105                 110

Asn Pro Ile Thr Arg Phe Val Ala Leu Phe Lys Glu Ser Glu Ser Pro
        115                 120                 125

Ile Val Ser Thr Val Asp Pro Ala Ala Phe Gly Pro Thr Leu Asp Arg
    130                 135                 140

Met Val Gly Glu Leu Tyr Arg Asp Pro Ile Ser Gly Asn Leu His Ile
145                 150                 155                 160

Asp Ala Gly Thr Leu Val Val Asn Asp Thr Ile Asp Gly Gln Ala Val
                165                 170                 175

Asp Arg Thr Ile Leu Glu Gln Ala Val Thr Glu Asn Trp Leu Asn Pro
            180                 185                 190

Glu Gly Val Lys Ala Glu Pro Tyr Val Val Pro Ala Ala Ile Ser Gln
```

```
        195                 200                 205

Asp Thr Ile Asp Lys Leu Ala Glu Gly Ala Gly Ala Lys Ala Val Ser
    210                 215                 220

Ser Pro Phe Val Val Arg Gly Asp Asp Gly Ile Glu Gly Thr Ile Pro
225                 230                 235                 240

Val Glu Arg Met Gly Glu Val Val Ser Phe Pro Glu Glu Asn Gly Thr
                245                 250                 255

Ile Arg Val Asp Ile Asn Ala Glu Ala Ala Thr Ala Met Leu Ala Glu
            260                 265                 270

Gly Leu Lys Glu Thr Glu Ile Glu Pro Thr Asn Ala Gln Ile Ser Phe
        275                 280                 285

Ser Ser Gly Ser Arg Val Val Thr Pro Glu Val Thr Gly His Gly Ile
    290                 295                 300

Asn Trp Glu Glu Thr Leu Ala Asp Leu Pro Asn Asn Leu Thr Gly Asp
305                 310                 315                 320

Gly Pro Arg Thr Ile Asp Ala Ile Tyr Glu Asp Thr Pro Ala Thr Phe
                325                 330                 335

Thr Ala Thr Asp Ala Gln Asn Ala Thr Phe Asn Glu Val Met Gly Glu
            340                 345                 350

Phe Thr Thr Gly Gly Phe Ser Ala Ala Ser Gly Thr Asn Ile Arg Leu
        355                 360                 365

Thr Ala Gln Met Val Asp Gly Ala Val Val Ser Pro Gly Asp Thr Phe
    370                 375                 380

Ser Leu
385
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<210> 2801
<211> 1545
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1522)
<223> RXA02576

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gctgatgagc actgtgaata aactcaggag ttaaatcctt atg acc ccg acc cgc 115
                                              Met Thr Pro Thr Arg
                                                1   5

cgt atc ctg ctg tgg gca tgg acg act gtg ctt ttg ggt tct ttg ctg 163
Arg Ile Leu Leu Trp Ala Trp Thr Thr Val Leu Leu Gly Ser Leu Leu
                10   15   20

tgg ccg ttg gct gcg cct ggc gag ttg ttg ttg cgg gat atg tcg gtg 211

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Trp Pro Leu Ala Ala Pro Gly Glu Leu Leu Leu Arg Asp Met Ser Val
            25                  30                  35

gtg gac cat cct gcg ttg tcg ttg aat gcg ttg ggt ttt ggt gat ttg   259
Val Asp His Pro Ala Leu Ser Leu Asn Ala Leu Gly Phe Gly Asp Leu
        40                  45                  50

ccg tcg cgg aac gcc ccg cag gat ggt gtg ctg gcg ttg ctt ggc ttt   307
Pro Ser Arg Asn Ala Pro Gln Asp Gly Val Leu Ala Leu Leu Gly Phe
    55                  60                  65

ttg ccg gtg agt tgg atc gtt cga acc atg ctg ctt gtg gcg ggt ttc   355
Leu Pro Val Ser Trp Ile Val Arg Thr Met Leu Leu Val Ala Gly Phe
70                  75                  80                  85

gcg ggc gcg tgg ggt gcg atg cgc ctt ggg cct tcc aag ttt ttg gcc   403
Ala Gly Ala Trp Gly Ala Met Arg Leu Gly Pro Ser Lys Phe Leu Ala
                90                  95                  100

gtt acc gtg gcg att tac aat ccc ttc gtg gtg gag cgt ctg ctg cag   451
Val Thr Val Ala Ile Tyr Asn Pro Phe Val Val Glu Arg Leu Leu Gln
            105                 110                 115

ggc cat tgg tcg ttg gtg atg gcg gtg tgg ctg ttc ccg ctg gtt gtg   499
Gly His Trp Ser Leu Val Met Ala Val Trp Leu Phe Pro Leu Val Val
        120                 125                 130

gcg ctg cgc agg cat ccg cgt tgg cag gtt gtg gcg atc tgg gcg gcg   547
Ala Leu Arg Arg His Pro Arg Trp Gln Val Val Ala Ile Trp Ala Ala
    135                 140                 145

tcg ttg acg ccc acg ggt gcg gtg gtt gcg gcg gtc acg ggc gtg gcg   595
Ser Leu Thr Pro Thr Gly Ala Val Val Ala Ala Val Thr Gly Val Ala
150                 155                 160                 165

agt tct aaa aga aaa cgc ttt acg acg cta tgt tcc ttc ctt tcg tgg   643
Ser Ser Lys Arg Lys Arg Phe Thr Thr Leu Cys Ser Phe Leu Ser Trp
                170                 175                 180

ctt cct tgg cta ata cct gcg ctt ctt gcc acc ccc act tcg gga ggt   691
Leu Pro Trp Leu Ile Pro Ala Leu Leu Ala Thr Pro Thr Ser Gly Gly
            185                 190                 195

gcg ctg acc ttc gcc att cgt tct gaa aca tat gca gga acg ttg gga   739
Ala Leu Thr Phe Ala Ile Arg Ser Glu Thr Tyr Ala Gly Thr Leu Gly
        200                 205                 210

act gcg ctg ggc ctg ggt gga att tgg aac gcg ggg gcc gtg ccg gcc   787
Thr Ala Leu Gly Leu Gly Gly Ile Trp Asn Ala Gly Ala Val Pro Ala
    215                 220                 225

tca cgc gaa ctg ggt ttc gcg gtt gct gga att ttg tta ttt gcg att   835
Ser Arg Glu Leu Gly Phe Ala Val Ala Gly Ile Leu Leu Phe Ala Ile
230                 235                 240                 245

ctg ctg gcg ggt ttc aaa aac tgt ccg tgg gtt ctc gca ctg ctg gcg   883
Leu Leu Ala Gly Phe Lys Asn Cys Pro Trp Val Leu Ala Leu Leu Ala
                250                 255                 260

gtc gta ggt ttt atg ggg gcg atc ggt ccg tgg ctg atg ccg aat ctg   931
Val Val Gly Phe Met Gly Ala Ile Gly Pro Trp Leu Met Pro Asn Leu
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            265                 270                 275

ttc acg tgg acc atc gca tat gtt cca ggc gcc gcg ctg ttt agg gat   979
Phe Thr Trp Thr Ile Ala Tyr Val Pro Gly Ala Ala Leu Phe Arg Asp
        280                 285                 290

tct caa aaa ctc ctc atg ctg gct atc cct gcc tat gtg tgt ttg gcc   1027
Ser Gln Lys Leu Leu Met Leu Ala Ile Pro Ala Tyr Val Cys Leu Ala
    295                 300                 305

gcc ggg gtg aaa agc cca ctg tcg tgg gtg gct acc ggt ttg gcg ttg   1075
Ala Gly Val Lys Ser Pro Leu Ser Trp Val Ala Thr Gly Leu Ala Leu
310                 315                 320                 325

ctc cag att cct gat gca cca cgt gag gtt tcc gtg ata cgc cca agt   1123
Leu Gln Ile Pro Asp Ala Pro Arg Glu Val Ser Val Ile Arg Pro Ser
                330                 335                 340

tca gcg cat gtg gaa tca gtg gaa gca ctg gca gaa atc gct gat ggc   1171
Ser Ala His Val Glu Ser Val Glu Ala Leu Ala Glu Ile Ala Asp Gly
            345                 350                 355

cgc gac atc tta atc atc ggc caa ggc ccc ttg gtg acc cgc gag gat   1219
Arg Asp Ile Leu Ile Ile Gly Gln Gly Pro Leu Val Thr Arg Glu Asp
        360                 365                 370

ggg atc ccg gtt gtc gat ccc aaa acc aaa gcc ctc tcc gtg gtg gaa   1267
Gly Ile Pro Val Val Asp Pro Lys Thr Lys Ala Leu Ser Val Val Glu
    375                 380                 385

tcc ggc gaa ctg cgt gtg gac gga atc atc acc gac gcg ccc tca cag   1315
Ser Gly Glu Leu Arg Val Asp Gly Ile Ile Thr Asp Ala Pro Ser Gln
390                 395                 400                 405

cgg tgg acc gaa gca acg cag gca tgg gcg gcc ggg gat atc gag cgc   1363
Arg Trp Thr Glu Ala Thr Gln Ala Trp Ala Ala Gly Asp Ile Glu Arg
                410                 415                 420

ctt gaa gaa ctt ggc gtt ggt gtc gtg gtg gat gga gat acg atc aca   1411
Leu Glu Glu Leu Gly Val Gly Val Val Val Asp Gly Asp Thr Ile Thr
            425                 430                 435

gaa act ggc gca cca ccg cag cat ggc tgg aaa tac tac ctc ggt gtg   1459
Glu Thr Gly Ala Pro Pro Gln His Gly Trp Lys Tyr Tyr Leu Gly Val
        440                 445                 450

ggc ctg acc gtg ctg tgg atg gcg ttg ccg ctg gga cta ctt ttt cga   1507
Gly Leu Thr Val Leu Trp Met Ala Leu Pro Leu Gly Leu Leu Phe Arg
    455                 460                 465

cgc aag acc aag aag tagttcctcg aactgcgctc ccg                    1545
Arg Lys Thr Lys Lys
470
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<210> 2802
<211> 474
<212> PRT
<213> Corynebacterium glutamicum

<400> 2802

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Met Thr Pro Thr Arg Arg Ile Leu Leu Trp Ala Trp Thr Thr Val Leu
 1               5                  10                  15

Leu Gly Ser Leu Leu Trp Pro Leu Ala Ala Pro Gly Glu Leu Leu Leu
            20                  25                  30

Arg Asp Met Ser Val Val Asp His Pro Ala Leu Ser Leu Asn Ala Leu
        35                  40                  45

Gly Phe Gly Asp Leu Pro Ser Arg Asn Ala Pro Gln Asp Gly Val Leu
    50                  55                  60

Ala Leu Leu Gly Phe Leu Pro Val Ser Trp Ile Val Arg Thr Met Leu
65                  70                  75                  80

Leu Val Ala Gly Phe Ala Gly Ala Trp Gly Ala Met Arg Leu Gly Pro
                85                  90                  95

Ser Lys Phe Leu Ala Val Thr Val Ala Ile Tyr Asn Pro Phe Val Val
            100                 105                 110

Glu Arg Leu Leu Gln Gly His Trp Ser Leu Val Met Ala Val Trp Leu
        115                 120                 125

Phe Pro Leu Val Val Ala Leu Arg Arg His Pro Arg Trp Gln Val Val
    130                 135                 140

Ala Ile Trp Ala Ala Ser Leu Thr Pro Thr Gly Ala Val Val Ala Ala
145                 150                 155                 160

Val Thr Gly Val Ala Ser Ser Lys Arg Lys Arg Phe Thr Thr Leu Cys
                165                 170                 175

Ser Phe Leu Ser Trp Leu Pro Trp Leu Ile Pro Ala Leu Leu Ala Thr
            180                 185                 190

Pro Thr Ser Gly Gly Ala Leu Thr Phe Ala Ile Arg Ser Glu Thr Tyr
        195                 200                 205

Ala Gly Thr Leu Gly Thr Ala Leu Gly Leu Gly Gly Ile Trp Asn Ala
    210                 215                 220

Gly Ala Val Pro Ala Ser Arg Glu Leu Gly Phe Ala Val Ala Gly Ile
225                 230                 235                 240

Leu Leu Phe Ala Ile Leu Leu Ala Gly Phe Lys Asn Cys Pro Trp Val
                245                 250                 255

Leu Ala Leu Leu Ala Val Val Gly Phe Met Gly Ala Ile Gly Pro Trp
            260                 265                 270

Leu Met Pro Asn Leu Phe Thr Trp Thr Ile Ala Tyr Val Pro Gly Ala
        275                 280                 285

Ala Leu Phe Arg Asp Ser Gln Lys Leu Leu Met Leu Ala Ile Pro Ala
    290                 295                 300

Tyr Val Cys Leu Ala Ala Gly Val Lys Ser Pro Leu Ser Trp Val Ala
305                 310                 315                 320

Thr Gly Leu Ala Leu Leu Gln Ile Pro Asp Ala Pro Arg Glu Val Ser
```

```
                325                 330                 335

Val Ile Arg Pro Ser Ser Ala His Val Glu Ser Val Glu Ala Leu Ala
            340                 345                 350

Glu Ile Ala Asp Gly Arg Asp Ile Leu Ile Ile Gly Gln Gly Pro Leu
        355                 360                 365

Val Thr Arg Glu Asp Gly Ile Pro Val Val Asp Pro Lys Thr Lys Ala
    370                 375                 380

Leu Ser Val Val Glu Ser Gly Glu Leu Arg Val Asp Gly Ile Ile Thr
385                 390                 395                 400

Asp Ala Pro Ser Gln Arg Trp Thr Glu Ala Thr Gln Ala Trp Ala Ala
                405                 410                 415

Gly Asp Ile Glu Arg Leu Glu Glu Leu Gly Val Gly Val Val Val Asp
            420                 425                 430

Gly Asp Thr Ile Thr Glu Thr Gly Ala Pro Pro Gln His Gly Trp Lys
        435                 440                 445

Tyr Tyr Leu Gly Val Gly Leu Thr Val Leu Trp Met Ala Leu Pro Leu
    450                 455                 460

Gly Leu Leu Phe Arg Arg Lys Thr Lys Lys
465                 470


<210> 2803
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<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(985)
<223> RXA02577

<400> 2803
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gcgtagtccc tcgagtgagc tgatgaatcc gcgatggcgg atg ggt gca tat gat   115
                                              Met Gly Ala Tyr Asp
                                                1               5

tgg gta gac att att tca aca tgc gag ttt agc gga aag gtg tgg gct   163
Trp Val Asp Ile Ile Ser Thr Cys Glu Phe Ser Gly Lys Val Trp Ala
                10                  15                  20

gtt ttt atg aag cga tct gca acg gtc ctc att att gcg ggc gtg ctg   211
Val Phe Met Lys Arg Ser Ala Thr Val Leu Ile Ile Ala Gly Val Leu
            25                  30                  35

ttc ctc att ttt gcc ttc acg gta ccg ccg tat gtg act ggt cag gcg   259
Phe Leu Ile Phe Ala Phe Thr Val Pro Pro Tyr Val Thr Gly Gln Ala
        40                  45                  50

cgg acg att ccg aag gat ttg gat ctg acg ttg gtg agc gaa agt ccg   307
Arg Thr Ile Pro Lys Asp Leu Asp Leu Thr Leu Val Ser Glu Ser Pro
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```
     55                  60                  65

cag ggg ttt gtg cgc act gaa cat att gtg act gct ccg acg gaa aag   355
Gln Gly Phe Val Arg Thr Glu His Ile Val Thr Ala Pro Thr Glu Lys
 70                  75                  80                  85

gtc gat gag atc gcg acg cat gtg gat cag aca gtt acg gat gtg cag   403
Val Asp Glu Ile Ala Thr His Val Asp Gln Thr Val Thr Asp Val Gln
                90                  95                 100

ggg aaa act gtt gcg gaa att tcg gat gat gtg gtg ttg att gga cac   451
Gly Lys Thr Val Ala Glu Ile Ser Asp Asp Val Val Leu Ile Gly His
            105                 110                 115

tct cgt tat ccg gtg att aag ccg act gcc acc att tcg ggt tcg ccg   499
Ser Arg Tyr Pro Val Ile Lys Pro Thr Ala Thr Ile Ser Gly Ser Pro
        120                 125                 130

gcg gat agt agc aat gtg gtg cgg gag ggg ttg cat tac ttc ttc ccg   547
Ala Asp Ser Ser Asn Val Val Arg Glu Gly Leu His Tyr Phe Phe Pro
    135                 140                 145

gct aat acg ttg cgg aat tct tat ccc tat tat gac atc gta ttg ggt   595
Ala Asn Thr Leu Arg Asn Ser Tyr Pro Tyr Tyr Asp Ile Val Leu Gly
150                 155                 160                 165

gag gat tcc ccg gtg gat tat gtc tcg cgc gag ggc aat act tat acc   643
Glu Asp Ser Pro Val Asp Tyr Val Ser Arg Glu Gly Asn Thr Tyr Thr
                170                 175                 180

ttc tac cag cat ctt cgt tat gtt cca ttg gat gat tct cac acc tat   691
Phe Tyr Gln His Leu Arg Tyr Val Pro Leu Asp Asp Ser His Thr Tyr
            185                 190                 195

tcg gtg gag cgg acc ctg aaa gtg gat cgt ttt tcc ggc atc att gtg   739
Ser Val Glu Arg Thr Leu Lys Val Asp Arg Phe Ser Gly Ile Ile Val
        200                 205                 210

gct aaa gat gag gcg atg acg ttt cat ggc cca gac ggc gat gac aca   787
Ala Lys Asp Glu Ala Met Thr Phe His Gly Pro Asp Gly Asp Asp Thr
    215                 220                 225

gta gaa ttc act tat act gcg gat acg ttg aag ctt ctg cag gat cat   835
Val Glu Phe Thr Tyr Thr Ala Asp Thr Leu Lys Leu Leu Gln Asp His
230                 235                 240                 245

gcg cat gat att gat cag cgg ttg tcg tgg gct aag ggg ttt gat ttc   883
Ala His Asp Ile Asp Gln Arg Leu Ser Trp Ala Lys Gly Phe Asp Phe
                250                 255                 260

ttt tct aaa ttc tta ggc ctg tcg ttg ctt gcg att ggt gtg ttc ctc   931
Phe Ser Lys Phe Leu Gly Leu Ser Leu Leu Ala Ile Gly Val Phe Leu
            265                 270                 275

acg gga att ttc aag cgc ggc cag ctg atg agc act gtg aat aaa ctc   979
Thr Gly Ile Phe Lys Arg Gly Gln Leu Met Ser Thr Val Asn Lys Leu
        280                 285                 290

agg agt taaatcctta tgaccccgac ccg                                1008
Arg Ser
    295
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<210> 2804
<211> 295
<212> PRT
<213> Corynebacterium glutamicum

<400> 2804

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Met Gly Ala Tyr Asp Trp Val Asp Ile Ile Ser Thr Cys Glu Phe Ser
  1               5                  10                  15

Gly Lys Val Trp Ala Val Phe Met Lys Arg Ser Ala Thr Val Leu Ile
             20                  25                  30

Ile Ala Gly Val Leu Phe Leu Ile Phe Ala Phe Thr Val Pro Pro Tyr
         35                  40                  45

Val Thr Gly Gln Ala Arg Thr Ile Pro Lys Asp Leu Asp Leu Thr Leu
     50                  55                  60

Val Ser Glu Ser Pro Gln Gly Phe Val Arg Thr Glu His Ile Val Thr
 65                  70                  75                  80

Ala Pro Thr Glu Lys Val Asp Glu Ile Ala Thr His Val Asp Gln Thr
                 85                  90                  95

Val Thr Asp Val Gln Gly Lys Thr Val Ala Glu Ile Ser Asp Asp Val
            100                 105                 110

Val Leu Ile Gly His Ser Arg Tyr Pro Val Ile Lys Pro Thr Ala Thr
        115                 120                 125

Ile Ser Gly Ser Pro Ala Asp Ser Ser Asn Val Val Arg Glu Gly Leu
    130                 135                 140

His Tyr Phe Phe Pro Ala Asn Thr Leu Arg Asn Ser Tyr Pro Tyr Tyr
145                 150                 155                 160

Asp Ile Val Leu Gly Glu Asp Ser Pro Val Asp Tyr Val Ser Arg Glu
                165                 170                 175

Gly Asn Thr Tyr Thr Phe Tyr Gln His Leu Arg Tyr Val Pro Leu Asp
            180                 185                 190

Asp Ser His Thr Tyr Ser Val Glu Arg Thr Leu Lys Val Asp Arg Phe
        195                 200                 205

Ser Gly Ile Ile Val Ala Lys Asp Glu Ala Met Thr Phe His Gly Pro
    210                 215                 220

Asp Gly Asp Asp Thr Val Glu Phe Thr Tyr Thr Ala Asp Thr Leu Lys
225                 230                 235                 240

Leu Leu Gln Asp His Ala His Asp Ile Asp Gln Arg Leu Ser Trp Ala
                245                 250                 255

Lys Gly Phe Asp Phe Phe Ser Lys Phe Leu Gly Leu Ser Leu Leu Ala
            260                 265                 270

Ile Gly Val Phe Leu Thr Gly Ile Phe Lys Arg Gly Gln Leu Met Ser
        275                 280                 285
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Thr Val Asn Lys Leu Arg Ser
    290                 295


<210> 2805
<211> 474
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(451)
<223> RXA02584

<400> 2805
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gacagtccgc aattgaaagg ccagatacgt gaaccgctgg atg tcc ttg ctg tgt   115
                                        Met Ser Leu Leu Cys
                                          1               5


gat tcc atc gcc atc ggt ctc ttc gca ctc ttc gcc cgc gtc gcc cac   163
Asp Ser Ile Ala Ile Gly Leu Phe Ala Leu Phe Ala Arg Val Ala His
                 10                  15                  20

caa agc gcc gac atg cca cta aat gtg cag ggc tgg ttt ttc aca tgg   211
Gln Ser Ala Asp Met Pro Leu Asn Val Gln Gly Trp Phe Phe Thr Trp
             25                  30                  35

ctg cca ttc ctc gca ggt gtg ttc atc gcc tac ctg gtg gca atc ctc   259
Leu Pro Phe Leu Ala Gly Val Phe Ile Ala Tyr Leu Val Ala Ile Leu
         40                  45                  50

cct gcg aag ctt ccc agc gaa cgc atc cgc ccc gct ggc ctg acc gtg   307
Pro Ala Lys Leu Pro Ser Glu Arg Ile Arg Pro Ala Gly Leu Thr Val
     55                  60                  65

tgg ata ctc gcg gta att gtg gga ctt gtg att tgg ggc ttc aac aat   355
Trp Ile Leu Ala Val Ile Val Gly Leu Val Ile Trp Gly Phe Asn Asn
 70                  75                  80                  85

ggt ggg gtt cca cac tgg tcc ttc atg att gtc gca acg acc gcc tcc   403
Gly Gly Val Pro His Trp Ser Phe Met Ile Val Ala Thr Thr Ala Ser
                 90                  95                 100

gcc att ttg gtt ctc ggc tgg cga gcg ttg ttt aag gtg aca atg cgc   451
Ala Ile Leu Val Leu Gly Trp Arg Ala Leu Phe Lys Val Thr Met Arg
            105                 110                 115

taagtgcttt taaaaaatgg gag                                        474


<210> 2806
<211> 117
<212> PRT
<213> Corynebacterium glutamicum

<400> 2806
Met Ser Leu Leu Cys Asp Ser Ile Ala Ile Gly Leu Phe Ala Leu Phe
  1               5                  10                  15
```

```
Ala Arg Val Ala His Gln Ser Ala Asp Met Pro Leu Asn Val Gln Gly
             20                  25                  30

Trp Phe Phe Thr Trp Leu Pro Phe Leu Ala Gly Val Phe Ile Ala Tyr
         35                  40                  45

Leu Val Ala Ile Leu Pro Ala Lys Leu Pro Ser Glu Arg Ile Arg Pro
     50                  55                  60

Ala Gly Leu Thr Val Trp Ile Leu Ala Val Ile Val Gly Leu Val Ile
 65                  70                  75                  80

Trp Gly Phe Asn Asn Gly Gly Val Pro His Trp Ser Phe Met Ile Val
                 85                  90                  95

Ala Thr Thr Ala Ser Ala Ile Leu Val Leu Gly Trp Arg Ala Leu Phe
            100                 105                 110

Lys Val Thr Met Arg
        115
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US20240327875A1

<210> 2807
<211> 1104
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1081)
<223> RXA02585

<400> 2807

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gcgaggattt ttcagcaacc cctggattcg ttgggctttg tccctggcgt ttctaggggt 60

gatcctattt ttcctgaggg atcagctgga tttcctcaaa atg ggc atc caa caa   115
                                            Met Gly Ile Gln Gln
                                              1               5

atc cgc cac gtc agc ccc gta ggc gtt gcc ctc acc atg gtg gcg ttg   163
Ile Arg His Val Ser Pro Val Gly Val Ala Leu Thr Met Val Ala Leu
                10                  15                  20

gtg ttg tca ttc gtt gcg atg gcc aga gtc atg cag atc atg ttg aaa   211
Val Leu Ser Phe Val Ala Met Ala Arg Val Met Gln Ile Met Leu Lys
            25                  30                  35

gcc gga ggt agt cct gcg act ctc aaa gcc acc acg gct tta act ttt   259
Ala Gly Gly Ser Pro Ala Thr Leu Lys Ala Thr Thr Ala Leu Thr Phe
        40                  45                  50

gcg gct aac tcc tgg tcc gcg acc ctt cct ggc ggc ccg gcg ttt tcc   307
Ala Ala Asn Ser Trp Ser Ala Thr Leu Pro Gly Gly Pro Ala Phe Ser
    55                  60                  65

gcg att ctc acc tat aaa gtg cag cgc agc tgg ggt gcc agc gcc gtg   355
Ala Ile Leu Thr Tyr Lys Val Gln Arg Ser Trp Gly Ala Ser Ala Val
70                  75                  80                  85

ctg tgt tcg tgg ttt ttc ctg ctc tcc agt gcc cta tcg acc gtc tgg   403
```

```
Leu Cys Ser Trp Phe Phe Leu Leu Ser Ser Ala Leu Ser Thr Val Trp
                 90                  95                 100

ttg gtt gct ctc ggt gtc atc gcc gtg ttt tat atg ggc gca tcg ctg   451
Leu Val Ala Leu Gly Val Ile Ala Val Phe Tyr Met Gly Ala Ser Leu
            105                 110                 115

aac tta tgg tca ctg atc gcc aca ttc atc gcc atg gtc ggg ctg tct   499
Asn Leu Trp Ser Leu Ile Ala Thr Phe Ile Ala Met Val Gly Leu Ser
        120                 125                 130

ggc gcc gtt tat tgg gca gcc aac aac ccc gac tcc ttg gct cgg tgg   547
Gly Ala Val Tyr Trp Ala Ala Asn Asn Pro Asp Ser Leu Ala Arg Trp
    135                 140                 145

gtg cga aaa ttg acg aaa aac agg gag tgg ggc ttc gtc gaa aag ctt   595
Val Arg Lys Leu Thr Lys Asn Arg Glu Trp Gly Phe Val Glu Lys Leu
150                 155                 160                 165

ctt gga agc att gag cag ctg cgc tcg gtc tcg ctc acc ggg ccg caa   643
Leu Gly Ser Ile Glu Gln Leu Arg Ser Val Ser Leu Thr Gly Pro Gln
                170                 175                 180

ttc gcg gcc agc acc gcg tgg tct tta ggc aat agg ctt ttc gac gcc   691
Phe Ala Ala Ser Thr Ala Trp Ser Leu Gly Asn Arg Leu Phe Asp Ala
            185                 190                 195

atc tcc ctc tgg att tgc atc tgg gcg gtc acc ggc act gcc ccg atg   739
Ile Ser Leu Trp Ile Cys Ile Trp Ala Val Thr Gly Thr Ala Pro Met
        200                 205                 210

ttt gaa cca gaa ccc aac aac acc acc atc gca ggc gta ctg ttg gcg   787
Phe Glu Pro Glu Pro Asn Asn Thr Thr Ile Ala Gly Val Leu Leu Ala
    215                 220                 225

tac acc acc gca aaa atc gca ggc tca atc caa gcc acc cca ggc gga   835
Tyr Thr Thr Ala Lys Ile Ala Gly Ser Ile Gln Ala Thr Pro Gly Gly
230                 235                 240                 245

atc ggc ccc atc gaa gcc gcc tac atc gca gcc ctc gta gcc acc ggt   883
Ile Gly Pro Ile Glu Ala Ala Tyr Ile Ala Ala Leu Val Ala Thr Gly
                250                 255                 260

atg acc gca gtg gaa gcc gcc gga gct gtc ata atc tac cgt tta tgc   931
Met Thr Ala Val Glu Ala Ala Gly Ala Val Ile Ile Tyr Arg Leu Cys
            265                 270                 275

tca ttt atc atc atg gcg att gtc gga tgg gtc atc tat ttt atc tat   979
Ser Phe Ile Ile Met Ala Ile Val Gly Trp Val Ile Tyr Phe Ile Tyr
        280                 285                 290

ttc acc ccc cag gga ctc aag gcc aat gaa tcc ctg gat gtg gaa cag   1027
Phe Thr Pro Gln Gly Leu Lys Ala Asn Glu Ser Leu Asp Val Glu Gln
    295                 300                 305

gat acg att aac tca gac tct aac cga cag tcc gca att gaa agg cca   1075
Asp Thr Ile Asn Ser Asp Ser Asn Arg Gln Ser Ala Ile Glu Arg Pro
310                 315                 320                 325

gat acg tgaaccgctg gatgtccttg ctg                                 1104
Asp Thr
```

<210> 2808
<211> 327
<212> PRT
<213> Corynebacterium glutamicum

<400> 2808
Met Gly Ile Gln Gln Ile Arg His Val Ser Pro Val Gly Val Ala Leu
1 5 10 15

Thr Met Val Ala Leu Val Leu Ser Phe Val Ala Met Ala Arg Val Met
20 25 30

Gln Ile Met Leu Lys Ala Gly Gly Ser Pro Ala Thr Leu Lys Ala Thr
35 40 45

Thr Ala Leu Thr Phe Ala Ala Asn Ser Trp Ser Ala Thr Leu Pro Gly
50 55 60

Gly Pro Ala Phe Ser Ala Ile Leu Thr Tyr Lys Val Gln Arg Ser Trp
65 70 75 80

Gly Ala Ser Ala Val Leu Cys Ser Trp Phe Phe Leu Leu Ser Ser Ala
85 90 95

Leu Ser Thr Val Trp Leu Val Ala Leu Gly Val Ile Ala Val Phe Tyr
100 105 110

Met Gly Ala Ser Leu Asn Leu Trp Ser Leu Ile Ala Thr Phe Ile Ala
115 120 125

Met Val Gly Leu Ser Gly Ala Val Tyr Trp Ala Ala Asn Asn Pro Asp
130 135 140

Ser Leu Ala Arg Trp Val Arg Lys Leu Thr Lys Asn Arg Glu Trp Gly
145 150 155 160

Phe Val Glu Lys Leu Leu Gly Ser Ile Glu Gln Leu Arg Ser Val Ser
165 170 175

Leu Thr Gly Pro Gln Phe Ala Ala Ser Thr Ala Trp Ser Leu Gly Asn
180 185 190

Arg Leu Phe Asp Ala Ile Ser Leu Trp Ile Cys Ile Trp Ala Val Thr
195 200 205

Gly Thr Ala Pro Met Phe Glu Pro Glu Pro Asn Asn Thr Thr Ile Ala
210 215 220

Gly Val Leu Leu Ala Tyr Thr Thr Ala Lys Ile Ala Gly Ser Ile Gln
225 230 235 240

Ala Thr Pro Gly Gly Ile Gly Pro Ile Glu Ala Ala Tyr Ile Ala Ala
245 250 255

Leu Val Ala Thr Gly Met Thr Ala Val Glu Ala Ala Gly Ala Val Ile
260 265 270

Ile Tyr Arg Leu Cys Ser Phe Ile Ile Met Ala Ile Val Gly Trp Val

```
        275                 280                 285

Ile Tyr Phe Ile Tyr Phe Thr Pro Gln Gly Leu Lys Ala Asn Glu Ser
    290                 295                 300

Leu Asp Val Glu Gln Asp Thr Ile Asn Ser Asp Ser Asn Arg Gln Ser
305                 310                 315                 320

Ala Ile Glu Arg Pro Asp Thr
                325
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<210> 2809
<211> 807
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(784)
<223> RXA02588

<400> 2809

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ctcagctgac tgaccgtcag gtcatcacca agtttgaagg caaaggcttg gaaaaagatc 60

acgtgatcaa tgagtacttg tggcagaagg tgcaaaacta atg tct gat gtg cat   115
                                              Met Ser Asp Val His
                                                1               5

gag gtc att cat agc tac aat ccc act gac aaa gaa ggc cct gaa agt   163
Glu Val Ile His Ser Tyr Asn Pro Thr Asp Lys Glu Gly Pro Glu Ser
                10                  15                  20

gtc ctt cta gtg tgg gac gct ccc aac cta gat atg ggt ttg ggc gct   211
Val Leu Leu Val Trp Asp Ala Pro Asn Leu Asp Met Gly Leu Gly Ala
            25                  30                  35

att ttg ggt ggt cgc cca acc gct gcg tac cga cct cgc ttt gat gcc   259
Ile Leu Gly Gly Arg Pro Thr Ala Ala Tyr Arg Pro Arg Phe Asp Ala
        40                  45                  50

atc ggt cgg tgg ttg ctt gct cgc gca ggt cgc agg gca cat gag ttg   307
Ile Gly Arg Trp Leu Leu Ala Arg Ala Gly Arg Arg Ala His Glu Leu
    55                  60                  65

ggc cgc cac att gag cct gag gca acg gtg ttt gcc aac atc acc cca   355
Gly Arg His Ile Glu Pro Glu Ala Thr Val Phe Ala Asn Ile Thr Pro
70                  75                  80                  85

ggt ggc tct gat gtt gtt cga cct tgg gtg gaa gcg ctg cgt aac gtt   403
Gly Gly Ser Asp Val Val Arg Pro Trp Val Glu Ala Leu Arg Asn Val
                90                  95                  100

ggt ttc gcg gtc ttc gct aag cct aag atc ggc gag gat tcc gat gtc   451
Gly Phe Ala Val Phe Ala Lys Pro Lys Ile Gly Glu Asp Ser Asp Val
            105                 110                 115

gat ccg gac atg att gat cac att cgc agg cgc tat gaa gaa ggc gtg   499
Asp Pro Asp Met Ile Asp His Ile Arg Arg Arg Tyr Glu Glu Gly Val
        120                 125                 130
```

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ctg cgg ggt gtc atc gtg gcc agt gca gat ggt cag aac ttc cgt gag   547
Leu Arg Gly Val Ile Val Ala Ser Ala Asp Gly Gln Asn Phe Arg Glu
    135                 140                 145

act ctc gag gag ctc gtt gca gag ggc att cct gcc acg gtc att ggt   595
Thr Leu Glu Glu Leu Val Ala Glu Gly Ile Pro Ala Thr Val Ile Gly
150                 155                 160                 165

ttc cac gag cac gcg tca tgg gct gta gct cat gac acc atc gag ttt   643
Phe His Glu His Ala Ser Trp Ala Val Ala His Asp Thr Ile Glu Phe
                170                 175                 180

gtt gat ctg gag gaa atc ccc ggc gtc ttc cgt gag ccg ctt cct cgc   691
Val Asp Leu Glu Glu Ile Pro Gly Val Phe Arg Glu Pro Leu Pro Arg
            185                 190                 195

gtc agc ctg gat aac ctg cca gac ggt ggc gca tgg ctg cag ccg ttc   739
Val Ser Leu Asp Asn Leu Pro Asp Gly Gly Ala Trp Leu Gln Pro Phe
        200                 205                 210

cgc cct ctg act gcc ttg tta tcc aac cgc cac aat tcc cag gag       784
Arg Pro Leu Thr Ala Leu Leu Ser Asn Arg His Asn Ser Gln Glu
    215                 220                 225

taatccaccc gtgttttcta aat                                        807


<210> 2810
<211> 228
<212> PRT
<213> Corynebacterium glutamicum

<400> 2810
Met Ser Asp Val His Glu Val Ile His Ser Tyr Asn Pro Thr Asp Lys
  1               5                  10                  15

Glu Gly Pro Glu Ser Val Leu Leu Val Trp Asp Ala Pro Asn Leu Asp
             20                  25                  30

Met Gly Leu Gly Ala Ile Leu Gly Gly Arg Pro Thr Ala Ala Tyr Arg
         35                  40                  45

Pro Arg Phe Asp Ala Ile Gly Arg Trp Leu Leu Ala Arg Ala Gly Arg
     50                  55                  60

Arg Ala His Glu Leu Gly Arg His Ile Glu Pro Glu Ala Thr Val Phe
 65                  70                  75                  80

Ala Asn Ile Thr Pro Gly Gly Ser Asp Val Val Arg Pro Trp Val Glu
                 85                  90                  95

Ala Leu Arg Asn Val Gly Phe Ala Val Phe Ala Lys Pro Lys Ile Gly
            100                 105                 110

Glu Asp Ser Asp Val Asp Pro Asp Met Ile Asp His Ile Arg Arg Arg
        115                 120                 125

Tyr Glu Glu Gly Val Leu Arg Gly Val Ile Val Ala Ser Ala Asp Gly
    130                 135                 140

Gln Asn Phe Arg Glu Thr Leu Glu Glu Leu Val Ala Glu Gly Ile Pro
```

```
145                 150                 155                 160

Ala Thr Val Ile Gly Phe His Glu His Ala Ser Trp Ala Val Ala His
                165                 170                 175

Asp Thr Ile Glu Phe Val Asp Leu Glu Glu Ile Pro Gly Val Phe Arg
            180                 185                 190

Glu Pro Leu Pro Arg Val Ser Leu Asp Asn Leu Pro Asp Gly Gly Ala
        195                 200                 205

Trp Leu Gln Pro Phe Arg Pro Leu Thr Ala Leu Leu Ser Asn Arg His
    210                 215                 220

Asn Ser Gln Glu
225
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Date Recue/Date Received 2020-04-20

<210> 2811
<211> 1953
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1930)
<223> RXA02591

<400> 2811

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atgtgtccgt tgtctcacct aaagttttaa ctagttctgt atctgaaagc tacgctaggg 60

ggcgagaact ctgtcgaatg acacaaaatc tggagaagta atg act act gct gca   115
                                            Met Thr Thr Ala Ala
                                              1               5

atc agg ggc ctt cag ggc gag gcg ccg acc aag aat aag gaa ctg ctg   163
Ile Arg Gly Leu Gln Gly Glu Ala Pro Thr Lys Asn Lys Glu Leu Leu
                10                  15                  20

aac tgg atc gca gac gcc gtc gag ctc ttc cag cct gag gct gtt gtg   211
Asn Trp Ile Ala Asp Ala Val Glu Leu Phe Gln Pro Glu Ala Val Val
            25                  30                  35

ttc gtt gat gga tcc cag gct gag tgg gat cgc atg gcg gag gat ctt   259
Phe Val Asp Gly Ser Gln Ala Glu Trp Asp Arg Met Ala Glu Asp Leu
        40                  45                  50

gtt gaa gcc ggt acc ctc atc aag ctc aac gag gaa aag cgt ccg aac   307
Val Glu Ala Gly Thr Leu Ile Lys Leu Asn Glu Glu Lys Arg Pro Asn
    55                  60                  65

agc tac cta gct cgt tcc aac cca tct gac gtt gcg cgc gtt gag tcc   355
Ser Tyr Leu Ala Arg Ser Asn Pro Ser Asp Val Ala Arg Val Glu Ser
70                  75                  80                  85

cgc acc ttc atc tgc tcc gag aag gaa gaa gat gct ggc cca acc aac   403
Arg Thr Phe Ile Cys Ser Glu Lys Glu Glu Asp Ala Gly Pro Thr Asn
                90                  95                  100

aac tgg gct cca cca cag gca atg aag gac gaa atg tcc aag cat tac   451
Asn Trp Ala Pro Pro Gln Ala Met Lys Asp Glu Met Ser Lys His Tyr
```

```
            105                 110                 115

gct ggt tcc atg aag ggg cgc acc atg tac gtc gtg cct ttc tgc atg   499
Ala Gly Ser Met Lys Gly Arg Thr Met Tyr Val Val Pro Phe Cys Met
        120                 125                 130

ggt cca atc agc gat ccg gac cct aag ctt ggt gtg cag ctc act gac   547
Gly Pro Ile Ser Asp Pro Asp Pro Lys Leu Gly Val Gln Leu Thr Asp
    135                 140                 145

tcc gag tac gtt gtc atg tcc atg cgc atc atg acc cgc atg ggt att   595
Ser Glu Tyr Val Val Met Ser Met Arg Ile Met Thr Arg Met Gly Ile
150                 155                 160                 165

gaa gcg ctg gac aag atc ggc gcg aac ggc agc ttc gtc agg tgc ctc   643
Glu Ala Leu Asp Lys Ile Gly Ala Asn Gly Ser Phe Val Arg Cys Leu
                170                 175                 180

cac tcc gtt ggt gct cct ttg gag cca ggc cag gaa gac gtt gca tgg   691
His Ser Val Gly Ala Pro Leu Glu Pro Gly Gln Glu Asp Val Ala Trp
            185                 190                 195

cct tgc aac gac acc aag tac atc acc cag ttc cca gag acc aag gaa   739
Pro Cys Asn Asp Thr Lys Tyr Ile Thr Gln Phe Pro Glu Thr Lys Glu
        200                 205                 210

att tgg tcc tac ggt tcc ggc tac ggc gga aac gca atc ctg gca aag   787
Ile Trp Ser Tyr Gly Ser Gly Tyr Gly Gly Asn Ala Ile Leu Ala Lys
    215                 220                 225

aag tgc tac gca ctg cgt atc gca tct gtc atg gct cgc gaa gaa gga   835
Lys Cys Tyr Ala Leu Arg Ile Ala Ser Val Met Ala Arg Glu Glu Gly
230                 235                 240                 245

tgg atg gct gag cac atg ctc atc ctg aag ctg atc aac cca gag ggc   883
Trp Met Ala Glu His Met Leu Ile Leu Lys Leu Ile Asn Pro Glu Gly
                250                 255                 260

aag gcg tac cac atc gca gca gca ttc cca tct gct tgt ggc aag acc   931
Lys Ala Tyr His Ile Ala Ala Ala Phe Pro Ser Ala Cys Gly Lys Thr
            265                 270                 275

aac ctc gcc atg atc act cca acc atc cca ggc tgg acc gct cag gtt   979
Asn Leu Ala Met Ile Thr Pro Thr Ile Pro Gly Trp Thr Ala Gln Val
        280                 285                 290

gtt ggc gac gac atc gct tgg ctg aag ctg cgc gag gac ggc ctc tac   1027
Val Gly Asp Asp Ile Ala Trp Leu Lys Leu Arg Glu Asp Gly Leu Tyr
    295                 300                 305

gca gtt aac cca gaa aat ggt ttc ttc ggt gtt gct cca ggc acc aac   1075
Ala Val Asn Pro Glu Asn Gly Phe Phe Gly Val Ala Pro Gly Thr Asn
310                 315                 320                 325

tac gca tcc aac cca atc gcg atg aag acc atg gaa cca ggc aac acc   1123
Tyr Ala Ser Asn Pro Ile Ala Met Lys Thr Met Glu Pro Gly Asn Thr
                330                 335                 340

ctg ttc acc aac gtg gca ctc acc gac gac ggc gac atc tgg tgg gaa   1171
Leu Phe Thr Asn Val Ala Leu Thr Asp Asp Gly Asp Ile Trp Trp Glu
            345                 350                 355
```

```
ggc atg gac ggc gac gcc cca gct cac ctc att gac tgg atg ggc aac   1219
Gly Met Asp Gly Asp Ala Pro Ala His Leu Ile Asp Trp Met Gly Asn
        360                 365                 370

gac tgg acc cca gag tcc gac gaa aac gct gct cac cct aac tcc cgt   1267
Asp Trp Thr Pro Glu Ser Asp Glu Asn Ala Ala His Pro Asn Ser Arg
    375                 380                 385

tac tgc gta gca atc gac cag tcc cca gca gca gca cct gag ttc aac   1315
Tyr Cys Val Ala Ile Asp Gln Ser Pro Ala Ala Ala Pro Glu Phe Asn
390                 395                 400                 405

gac tgg gaa ggc gtc aag atc gac gca atc ctc ttc ggt gga cgt cgc   1363
Asp Trp Glu Gly Val Lys Ile Asp Ala Ile Leu Phe Gly Gly Arg Arg
                410                 415                 420

gca gac acc gtc cca ctg gtt acc cag acc tac gac tgg gag cac ggc   1411
Ala Asp Thr Val Pro Leu Val Thr Gln Thr Tyr Asp Trp Glu His Gly
            425                 430                 435

acc atg gtt ggt gca ctg ctc gca tcc ggt cag acc gca gct tcc gca   1459
Thr Met Val Gly Ala Leu Leu Ala Ser Gly Gln Thr Ala Ala Ser Ala
        440                 445                 450

gaa gca aag gtc ggc aca ctc cgc cac gac cca atg gca atg ctc cca   1507
Glu Ala Lys Val Gly Thr Leu Arg His Asp Pro Met Ala Met Leu Pro
    455                 460                 465

ttc att ggc tac aac gct ggt gaa tac ctg cag aac tgg att gac atg   1555
Phe Ile Gly Tyr Asn Ala Gly Glu Tyr Leu Gln Asn Trp Ile Asp Met
470                 475                 480                 485

ggt aac aag ggt ggc gac aag atg cca tcc atc ttc ctg gtc aac tgg   1603
Gly Asn Lys Gly Gly Asp Lys Met Pro Ser Ile Phe Leu Val Asn Trp
                490                 495                 500

ttc cgc cgt ggc gaa gat gga cgc ttc ctg tgg cct ggc ttc ggc gac   1651
Phe Arg Arg Gly Glu Asp Gly Arg Phe Leu Trp Pro Gly Phe Gly Asp
            505                 510                 515

aac tct cgc gtt ctg aag tgg gtc atc gac cgc atc gaa ggc cac gtt   1699
Asn Ser Arg Val Leu Lys Trp Val Ile Asp Arg Ile Glu Gly His Val
        520                 525                 530

ggc gca gac gag acc gtt gtt gga cac acc gct aag gcc gaa gac ctc   1747
Gly Ala Asp Glu Thr Val Val Gly His Thr Ala Lys Ala Glu Asp Leu
    535                 540                 545

gac ctc gac ggc ctc gac acc cca att gag gat gtc aag gaa gca ctg   1795
Asp Leu Asp Gly Leu Asp Thr Pro Ile Glu Asp Val Lys Glu Ala Leu
550                 555                 560                 565

acc gct cct gca gag cag tgg gca aac gac gtt gaa gac aac gcc gag   1843
Thr Ala Pro Ala Glu Gln Trp Ala Asn Asp Val Glu Asp Asn Ala Glu
                570                 575                 580

tac ctc act ttc ctc gga cca cgt gtt cct gca gag gtt cac agc cag   1891
Tyr Leu Thr Phe Leu Gly Pro Arg Val Pro Ala Glu Val His Ser Gln
            585                 590                 595
```

```
ttc gat gct ctg aag gcc cgc att tca gca gct cac gct taaagttcac    1940
Phe Asp Ala Leu Lys Ala Arg Ile Ser Ala Ala His Ala
        600                 605                 610

gcttaagaac tgc                                                   1953


<210> 2812
<211> 610
<212> PRT
<213> Corynebacterium glutamicum

<400> 2812
Met Thr Thr Ala Ala Ile Arg Gly Leu Gln Gly Glu Ala Pro Thr Lys
  1               5                  10                  15

Asn Lys Glu Leu Leu Asn Trp Ile Ala Asp Ala Val Glu Leu Phe Gln
             20                  25                  30

Pro Glu Ala Val Val Phe Val Asp Gly Ser Gln Ala Glu Trp Asp Arg
         35                  40                  45

Met Ala Glu Asp Leu Val Glu Ala Gly Thr Leu Ile Lys Leu Asn Glu
     50                  55                  60

Glu Lys Arg Pro Asn Ser Tyr Leu Ala Arg Ser Asn Pro Ser Asp Val
 65                  70                  75                  80

Ala Arg Val Glu Ser Arg Thr Phe Ile Cys Ser Glu Lys Glu Glu Asp
                 85                  90                  95

Ala Gly Pro Thr Asn Asn Trp Ala Pro Pro Gln Ala Met Lys Asp Glu
            100                 105                 110

Met Ser Lys His Tyr Ala Gly Ser Met Lys Gly Arg Thr Met Tyr Val
        115                 120                 125

Val Pro Phe Cys Met Gly Pro Ile Ser Asp Pro Asp Pro Lys Leu Gly
    130                 135                 140

Val Gln Leu Thr Asp Ser Glu Tyr Val Val Met Ser Met Arg Ile Met
145                 150                 155                 160

Thr Arg Met Gly Ile Glu Ala Leu Asp Lys Ile Gly Ala Asn Gly Ser
                165                 170                 175

Phe Val Arg Cys Leu His Ser Val Gly Ala Pro Leu Glu Pro Gly Gln
            180                 185                 190

Glu Asp Val Ala Trp Pro Cys Asn Asp Thr Lys Tyr Ile Thr Gln Phe
        195                 200                 205

Pro Glu Thr Lys Glu Ile Trp Ser Tyr Gly Ser Gly Tyr Gly Gly Asn
    210                 215                 220

Ala Ile Leu Ala Lys Lys Cys Tyr Ala Leu Arg Ile Ala Ser Val Met
225                 230                 235                 240

Ala Arg Glu Glu Gly Trp Met Ala Glu His Met Leu Ile Leu Lys Leu
                245                 250                 255
```

```
Ile Asn Pro Glu Gly Lys Ala Tyr His Ile Ala Ala Ala Phe Pro Ser
            260                 265                 270

Ala Cys Gly Lys Thr Asn Leu Ala Met Ile Thr Pro Thr Ile Pro Gly
        275                 280                 285

Trp Thr Ala Gln Val Val Gly Asp Asp Ile Ala Trp Leu Lys Leu Arg
    290                 295                 300

Glu Asp Gly Leu Tyr Ala Val Asn Pro Glu Asn Gly Phe Phe Gly Val
305                 310                 315                 320

Ala Pro Gly Thr Asn Tyr Ala Ser Asn Pro Ile Ala Met Lys Thr Met
                325                 330                 335

Glu Pro Gly Asn Thr Leu Phe Thr Asn Val Ala Leu Thr Asp Asp Gly
            340                 345                 350

Asp Ile Trp Trp Glu Gly Met Asp Gly Asp Ala Pro Ala His Leu Ile
        355                 360                 365

Asp Trp Met Gly Asn Asp Trp Thr Pro Glu Ser Asp Glu Asn Ala Ala
    370                 375                 380

His Pro Asn Ser Arg Tyr Cys Val Ala Ile Asp Gln Ser Pro Ala Ala
385                 390                 395                 400

Ala Pro Glu Phe Asn Asp Trp Glu Gly Val Lys Ile Asp Ala Ile Leu
                405                 410                 415

Phe Gly Gly Arg Arg Ala Asp Thr Val Pro Leu Val Thr Gln Thr Tyr
            420                 425                 430

Asp Trp Glu His Gly Thr Met Val Gly Ala Leu Leu Ala Ser Gly Gln
        435                 440                 445

Thr Ala Ala Ser Ala Glu Ala Lys Val Gly Thr Leu Arg His Asp Pro
    450                 455                 460

Met Ala Met Leu Pro Phe Ile Gly Tyr Asn Ala Gly Glu Tyr Leu Gln
465                 470                 475                 480

Asn Trp Ile Asp Met Gly Asn Lys Gly Gly Asp Lys Met Pro Ser Ile
                485                 490                 495

Phe Leu Val Asn Trp Phe Arg Arg Gly Glu Asp Gly Arg Phe Leu Trp
            500                 505                 510

Pro Gly Phe Gly Asp Asn Ser Arg Val Leu Lys Trp Val Ile Asp Arg
        515                 520                 525

Ile Glu Gly His Val Gly Ala Asp Glu Thr Val Val Gly His Thr Ala
    530                 535                 540

Lys Ala Glu Asp Leu Asp Leu Asp Gly Leu Asp Thr Pro Ile Glu Asp
545                 550                 555                 560

Val Lys Glu Ala Leu Thr Ala Pro Ala Glu Gln Trp Ala Asn Asp Val
                565                 570                 575

Glu Asp Asn Ala Glu Tyr Leu Thr Phe Leu Gly Pro Arg Val Pro Ala
```

```
            580                 585                 590

Glu Val His Ser Gln Phe Asp Ala Leu Lys Ala Arg Ile Ser Ala Ala
        595                 600                 605

His Ala
    610


<210> 2813
<211> 714
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(691)
<223> RXA02598

<400> 2813
ctttgggaaa gtacccccta tgacggaaaa ctggatggat cctgtggttg aaccacagtc 60

aacgggagag gggaaatcgg acactatatg gttggagatc gtg aca act gac caa   115
                                            Val Thr Thr Asp Gln
                                              1               5

aac aaa aga agt ctc agt gag ctt gcg gcc aga atc gtt agt gaa atc   163
Asn Lys Arg Ser Leu Ser Glu Leu Ala Ala Arg Ile Val Ser Glu Ile
                10                  15                  20

tgt gca ccg tgg gta ctc aac atc gga ttt ttc ctc atc ctg ggc ggc   211
Cys Ala Pro Trp Val Leu Asn Ile Gly Phe Phe Leu Ile Leu Gly Gly
            25                  30                  35

gta aca ggc gcc tgg acg cta gga att gtg gcg gca atc gga acc gga   259
Val Thr Gly Ala Trp Thr Leu Gly Ile Val Ala Ala Ile Gly Thr Gly
        40                  45                  50

atc gtt ccg atg atc tta att ttg ggc ttg atg aag ctc ggc agg gta   307
Ile Val Pro Met Ile Leu Ile Leu Gly Leu Met Lys Leu Gly Arg Val
    55                  60                  65

gga aac cac cat gtg acg acc cga aat cag cgc ggc ctt gtg ttt gtg   355
Gly Asn His His Val Thr Thr Arg Asn Gln Arg Gly Leu Val Phe Val
70                  75                  80                  85

ggc atc att gtt tgt gtc atc att ttg att ttt atc ctc aga gcc ctt   403
Gly Ile Ile Val Cys Val Ile Ile Leu Ile Phe Ile Leu Arg Ala Leu
                90                  95                  100

gaa gca cct cag ctg att tgg gat ggc atg ttc tca gca ctg att ttc   451
Glu Ala Pro Gln Leu Ile Trp Asp Gly Met Phe Ser Ala Leu Ile Phe
            105                 110                 115

tta gtt ctg ttt gca caa gtg acg ttg aaa att aaa gcc tca gtt cat   499
Leu Val Leu Phe Ala Gln Val Thr Leu Lys Ile Lys Ala Ser Val His
        120                 125                 130

gtt ggg ctg tgg gtg tgt tta gtg atg ttc ctc ggt ctg acg gtt tct   547
Val Gly Leu Trp Val Cys Leu Val Met Phe Leu Gly Leu Thr Val Ser
    135                 140                 145
```

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tcg tgg tgg tta ctc ggg ttg ctg ttt acc cca gtc acc gcg tgg gca   595
Ser Trp Trp Leu Leu Gly Leu Leu Phe Thr Pro Val Thr Ala Trp Ala
150                 155                 160                 165

cgt atg cgg atc aag cat cat acg atg tcg gag att gtg gcg ggc gtt   643
Arg Met Arg Ile Lys His His Thr Met Ser Glu Ile Val Ala Gly Val
                170                 175                 180

gtt aca gga gca gtt gca acc ggc att tgt tat gca ctc cta ctt gcg   691
Val Thr Gly Ala Val Ala Thr Gly Ile Cys Tyr Ala Leu Leu Leu Ala
            185                 190                 195

taaaggagaa ttatggatca gct                                        714


<210> 2814
<211> 197
<212> PRT
<213> Corynebacterium glutamicum

<400> 2814
Val Thr Thr Asp Gln Asn Lys Arg Ser Leu Ser Glu Leu Ala Ala Arg
  1               5                  10                  15

Ile Val Ser Glu Ile Cys Ala Pro Trp Val Leu Asn Ile Gly Phe Phe
             20                  25                  30

Leu Ile Leu Gly Gly Val Thr Gly Ala Trp Thr Leu Gly Ile Val Ala
         35                  40                  45

Ala Ile Gly Thr Gly Ile Val Pro Met Ile Leu Ile Leu Gly Leu Met
     50                  55                  60

Lys Leu Gly Arg Val Gly Asn His His Val Thr Thr Arg Asn Gln Arg
 65                  70                  75                  80

Gly Leu Val Phe Val Gly Ile Ile Val Cys Val Ile Ile Leu Ile Phe
                 85                  90                  95

Ile Leu Arg Ala Leu Glu Ala Pro Gln Leu Ile Trp Asp Gly Met Phe
            100                 105                 110

Ser Ala Leu Ile Phe Leu Val Leu Phe Ala Gln Val Thr Leu Lys Ile
        115                 120                 125

Lys Ala Ser Val His Val Gly Leu Trp Val Cys Leu Val Met Phe Leu
    130                 135                 140

Gly Leu Thr Val Ser Ser Trp Trp Leu Leu Gly Leu Leu Phe Thr Pro
145                 150                 155                 160

Val Thr Ala Trp Ala Arg Met Arg Ile Lys His His Thr Met Ser Glu
                165                 170                 175

Ile Val Ala Gly Val Val Thr Gly Ala Val Ala Thr Gly Ile Cys Tyr
            180                 185                 190

Ala Leu Leu Leu Ala
        195
```

<210> 2815
<211> 1521
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1498)
<223> RXA02600

<400> 2815
gattttgctt ttcgacgcac cgttcggccg ttatctagat ctggtcacaa tgtcggtttt 60

tcatggattc atgtccttta tcggacgtac tgtggggagt atg caa cct ttt cca 115
Met Gln Pro Phe Pro
1 5

ctg tcc tta acc aac agc tcc gtc gct ggt att gca gcg gga gcg ttg 163
Leu Ser Leu Thr Asn Ser Ser Val Ala Gly Ile Ala Ala Gly Ala Leu
10 15 20

ctg ttt ctc tcc gtc cct ttc gca tcg cct gtt cac gcg caa acc ata 211
Leu Phe Leu Ser Val Pro Phe Ala Ser Pro Val His Ala Gln Thr Ile
25 30 35

ctg caa gac acc ctt gaa gtg act gtg ttg gat aat gcc gac gag ctc 259
Leu Gln Asp Thr Leu Glu Val Thr Val Leu Asp Asn Ala Asp Glu Leu
40 45 50

gct cca gag gat gag gat ttc ctc agc acg gaa aca ccc aag att gat 307
Ala Pro Glu Asp Glu Asp Phe Leu Ser Thr Glu Thr Pro Lys Ile Asp
55 60 65

ttc cct gac tca gtt acc gca gtc cgg tac atc acg ctc acg gac aac 355
Phe Pro Asp Ser Val Thr Ala Val Arg Tyr Ile Thr Leu Thr Asp Asn
70 75 80 85

act gac aaa atc aat gat gac gtt gaa aat tac ctg cgc gcc gaa cac 403
Thr Asp Lys Ile Asn Asp Asp Val Glu Asn Tyr Leu Arg Ala Glu His
90 95 100

ccc gag tgg atc caa aca aac tct ttc gcc cct ggt gaa gtg atc atc 451
Pro Glu Trp Ile Gln Thr Asn Ser Phe Ala Pro Gly Glu Val Ile Ile
105 110 115

gca gtc ggt ttc gac ccc aac acc atg ggt gcc tac gcg ggt aac gat 499
Ala Val Gly Phe Asp Pro Asn Thr Met Gly Ala Tyr Ala Gly Asn Asp
120 125 130

gtg gcc gca gag act ggg atc gca gaa caa gac cgc atc gac ggc acc 547
Val Ala Ala Glu Thr Gly Ile Ala Glu Gln Asp Arg Ile Asp Gly Thr
135 140 145

acc gat gcg atg cgc cca tta ctc caa gac ggt cgc att gcc cta ggc 595
Thr Asp Ala Met Arg Pro Leu Leu Gln Asp Gly Arg Ile Ala Leu Gly
150 155 160 165

atg ttg gag ggt gca aaa tcg gtt gct gat acc tct gtc gtt cgg gaa 643
Met Leu Glu Gly Ala Lys Ser Val Ala Asp Thr Ser Val Val Arg Glu
170 175 180

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agc tca gct cca agt ggt gga gta atc gcc gct att ttg ggt ggc atc   691
Ser Ser Ala Pro Ser Gly Gly Val Ile Ala Ala Ile Leu Gly Gly Ile
            185                 190                 195

gct gct ctc gtg gca att att gtc gcg tgg gct acg agt tac gcg aat   739
Ala Ala Leu Val Ala Ile Ile Val Ala Trp Ala Thr Ser Tyr Ala Asn
        200                 205                 210

aag aag aag gca gaa aag gct cgt gag cag ttt gat tat gca tca cgc   787
Lys Lys Lys Ala Glu Lys Ala Arg Glu Gln Phe Asp Tyr Ala Ser Arg
    215                 220                 225

cat tat ggt gag gtc gcc cag caa ctc gac ggt atc aac gtg cga gcg   835
His Tyr Gly Glu Val Ala Gln Gln Leu Asp Gly Ile Asn Val Arg Ala
230                 235                 240                 245

cac tcg cta act tcc cca ctg gct gat gat gag ctc cgc agg caa tgg   883
His Ser Leu Thr Ser Pro Leu Ala Asp Asp Glu Leu Arg Arg Gln Trp
                250                 255                 260

gac gat gta aat tct cgt ttt ctt gaa gtc aat gat att ttt ggc agg   931
Asp Asp Val Asn Ser Arg Phe Leu Glu Val Asn Asp Ile Phe Gly Arg
            265                 270                 275

ctc gaa ggt ttg acc tcg acc tca gaa aac aag gca ttt cga aaa gcc   979
Leu Glu Gly Leu Thr Ser Thr Ser Glu Asn Lys Ala Phe Arg Lys Ala
        280                 285                 290

ttg cca gat att gaa aaa gct cat act gcc gtg act caa atg gag atc   1027
Leu Pro Asp Ile Glu Lys Ala His Thr Ala Val Thr Gln Met Glu Ile
    295                 300                 305

gca cag aaa aac att gac acg ctc tac gat atg gag cac ggc cat gaa   1075
Ala Gln Lys Asn Ile Asp Thr Leu Tyr Asp Met Glu His Gly His Glu
310                 315                 320                 325

gac acc cgt cgc agg gaa tta act agg ctg cgt gcc gat atg cag gaa   1123
Asp Thr Arg Arg Arg Glu Leu Thr Arg Leu Arg Ala Asp Met Gln Glu
                330                 335                 340

gcc cgt caa gat atc aac gat aaa gat gca gtt gtt gac gat att ctc   1171
Ala Arg Gln Asp Ile Asn Asp Lys Asp Ala Val Val Asp Asp Ile Leu
            345                 350                 355

cgc acg ctg atc cag cgc acg gaa act atc gca ccg tcc gca cct gat   1219
Arg Thr Leu Ile Gln Arg Thr Glu Thr Ile Ala Pro Ser Ala Pro Asp
        360                 365                 370

ttc atg gac caa tac gcc cgc ttg atc cgt gat tat gcc gtg gcg ctt   1267
Phe Met Asp Gln Tyr Ala Arg Leu Ile Arg Asp Tyr Ala Val Ala Leu
    375                 380                 385

caa ggt gtg gaa aag aac ctc gag cag gtt aaa cag acc acc gag cgc   1315
Gln Gly Val Glu Lys Asn Leu Glu Gln Val Lys Gln Thr Thr Glu Arg
390                 395                 400                 405

aat gct cca gcc atc tac gac gac aat tgg cgc gtg ggc act ggc tac   1363
Asn Ala Pro Ala Ile Tyr Asp Asp Asn Trp Arg Val Gly Thr Gly Tyr
                410                 415                 420
```

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aac tcg tgg gtc ccg tac tac atg atc agt tct tgg cac gca gct gat   1411
Asn Ser Trp Val Pro Tyr Tyr Met Ile Ser Ser Trp His Ala Ala Asp
            425                 430                 435

gtc agt gct gca tcg tca gct tct tcc agt tca gca aat acc act ttc   1459
Val Ser Ala Ala Ser Ser Ala Ser Ser Ser Ser Ala Asn Thr Thr Phe
        440                 445                 450

agc agt ggt ttc agc ggc gct gga gga ggt tcc agc tgg taaacaccac    1508
Ser Ser Gly Phe Ser Gly Ala Gly Gly Gly Ser Ser Trp
    455                 460                 465

cactgaagtc aac                                                   1521


<210> 2816
<211> 466
<212> PRT
<213> Corynebacterium glutamicum

<400> 2816
Met Gln Pro Phe Pro Leu Ser Leu Thr Asn Ser Ser Val Ala Gly Ile
  1               5                  10                  15

Ala Ala Gly Ala Leu Leu Phe Leu Ser Val Pro Phe Ala Ser Pro Val
             20                  25                  30

His Ala Gln Thr Ile Leu Gln Asp Thr Leu Glu Val Thr Val Leu Asp
         35                  40                  45

Asn Ala Asp Glu Leu Ala Pro Glu Asp Glu Asp Phe Leu Ser Thr Glu
     50                  55                  60

Thr Pro Lys Ile Asp Phe Pro Asp Ser Val Thr Ala Val Arg Tyr Ile
 65                  70                  75                  80

Thr Leu Thr Asp Asn Thr Asp Lys Ile Asn Asp Asp Val Glu Asn Tyr
                 85                  90                  95

Leu Arg Ala Glu His Pro Glu Trp Ile Gln Thr Asn Ser Phe Ala Pro
            100                 105                 110

Gly Glu Val Ile Ile Ala Val Gly Phe Asp Pro Asn Thr Met Gly Ala
        115                 120                 125

Tyr Ala Gly Asn Asp Val Ala Ala Glu Thr Gly Ile Ala Glu Gln Asp
    130                 135                 140

Arg Ile Asp Gly Thr Thr Asp Ala Met Arg Pro Leu Leu Gln Asp Gly
145                 150                 155                 160

Arg Ile Ala Leu Gly Met Leu Glu Gly Ala Lys Ser Val Ala Asp Thr
                165                 170                 175

Ser Val Val Arg Glu Ser Ser Ala Pro Ser Gly Gly Val Ile Ala Ala
            180                 185                 190

Ile Leu Gly Gly Ile Ala Ala Leu Val Ala Ile Ile Val Ala Trp Ala
        195                 200                 205

Thr Ser Tyr Ala Asn Lys Lys Lys Ala Glu Lys Ala Arg Glu Gln Phe
```

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    210                 215                 220

Asp Tyr Ala Ser Arg His Tyr Gly Glu Val Ala Gln Gln Leu Asp Gly
225                 230                 235                 240

Ile Asn Val Arg Ala His Ser Leu Thr Ser Pro Leu Ala Asp Asp Glu
                245                 250                 255

Leu Arg Arg Gln Trp Asp Asp Val Asn Ser Arg Phe Leu Glu Val Asn
            260                 265                 270

Asp Ile Phe Gly Arg Leu Glu Gly Leu Thr Ser Thr Ser Glu Asn Lys
        275                 280                 285

Ala Phe Arg Lys Ala Leu Pro Asp Ile Glu Lys Ala His Thr Ala Val
    290                 295                 300

Thr Gln Met Glu Ile Ala Gln Lys Asn Ile Asp Thr Leu Tyr Asp Met
305                 310                 315                 320

Glu His Gly His Glu Asp Thr Arg Arg Arg Glu Leu Thr Arg Leu Arg
                325                 330                 335

Ala Asp Met Gln Glu Ala Arg Gln Asp Ile Asn Asp Lys Asp Ala Val
            340                 345                 350

Val Asp Asp Ile Leu Arg Thr Leu Ile Gln Arg Thr Glu Thr Ile Ala
        355                 360                 365

Pro Ser Ala Pro Asp Phe Met Asp Gln Tyr Ala Arg Leu Ile Arg Asp
    370                 375                 380

Tyr Ala Val Ala Leu Gln Gly Val Glu Lys Asn Leu Glu Gln Val Lys
385                 390                 395                 400

Gln Thr Thr Glu Arg Asn Ala Pro Ala Ile Tyr Asp Asp Asn Trp Arg
                405                 410                 415

Val Gly Thr Gly Tyr Asn Ser Trp Val Pro Tyr Tyr Met Ile Ser Ser
            420                 425                 430

Trp His Ala Ala Asp Val Ser Ala Ala Ser Ser Ala Ser Ser Ser Ser
        435                 440                 445

Ala Asn Thr Thr Phe Ser Ser Gly Phe Ser Gly Ala Gly Gly Gly Ser
    450                 455                 460

Ser Trp
465


<210> 2817
<211> 2112
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2089)
<223> RXA02601
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<400> 2817
ctcatacaat tgccaggatc ttccatggcg gatacggcgc gtaagttctg tgaatgcggg 60

gtccggatac tacgcttagg caagataaat tgtgagttca atg aag ggt gaa gat 115
Met Lys Gly Glu Asp
1 5

acg tca atg agc gca aca aac ctg gcg gtt gag cag cta cag cga gtg 163
Thr Ser Met Ser Ala Thr Asn Leu Ala Val Glu Gln Leu Gln Arg Val
10 15 20

ctc ctg ccg agg cgc ggc gag cca gca gat gtc agg tcg ttg tac ctg 211
Leu Leu Pro Arg Arg Gly Glu Pro Ala Asp Val Arg Ser Leu Tyr Leu
25 30 35

ttg gaa gca gaa agt aat aag gaa cgc ctg gaa tgg gaa gat cgt ttt 259
Leu Glu Ala Glu Ser Asn Lys Glu Arg Leu Glu Trp Glu Asp Arg Phe
40 45 50

agc gtt tcc gtc ccc gct ggc gcc gag gtg tct ttt cag acc tac ttc 307
Ser Val Ser Val Pro Ala Gly Ala Glu Val Ser Phe Gln Thr Tyr Phe
55 60 65

aat gca ttt cct gca agc tac tgg cgt cgc tgg tca cag cta gat tct 355
Asn Ala Phe Pro Ala Ser Tyr Trp Arg Arg Trp Ser Gln Leu Asp Ser
70 75 80 85

gtc gta ctg aaa ctg aaa gtt tcc ggc gaa gcg cgc gtc gac ctc tac 403
Val Val Leu Lys Leu Lys Val Ser Gly Glu Ala Arg Val Asp Leu Tyr
90 95 100

cga tcc aag atc gat gga gca cgc atc gga att acc ggt tcc gta gtc 451
Arg Ser Lys Ile Asp Gly Ala Arg Ile Gly Ile Thr Gly Ser Val Val
105 110 115

aaa gat gac ttc atc gaa ttt gaa gtt tca tta gcc cca ttc gaa gac 499
Lys Asp Asp Phe Ile Glu Phe Glu Val Ser Leu Ala Pro Phe Glu Asp
120 125 130

ggc ggc tgg atc tgg ttc gac ctc acc gct gaa acc gac gca acc gtc 547
Gly Gly Trp Ile Trp Phe Asp Leu Thr Ala Glu Thr Asp Ala Thr Val
135 140 145

gaa gaa gca ggc tgg tac gct cca cac gcg cca aaa gcc cag atc atg 595
Glu Glu Ala Gly Trp Tyr Ala Pro His Ala Pro Lys Ala Gln Ile Met
150 155 160 165

cca gat gga tct gaa gtc ggc cca ttt gaa gcc cgt gca acc gtc gga 643
Pro Asp Gly Ser Glu Val Gly Pro Phe Glu Ala Arg Ala Thr Val Gly
170 175 180

atc ccg acc ttc aac cgc cca gct gat gca gtt gca gca ctg gaa gca 691
Ile Pro Thr Phe Asn Arg Pro Ala Asp Ala Val Ala Ala Leu Glu Ala
185 190 195

ctt gcc tcc gac cca gca gtt gac gcc gtc att gat acc gtc atc atg 739
Leu Ala Ser Asp Pro Ala Val Asp Ala Val Ile Asp Thr Val Ile Met
200 205 210

cct gat caa ggc aac aag cac cct gcc gac gag cca ggt tac aag gca 787
Pro Asp Gln Gly Asn Lys His Pro Ala Asp Glu Pro Gly Tyr Lys Ala

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    215                 220                 225

gct gtt gag cac ttc ggc gac cgc ttc ttc gaa ttc cgc cag ggc aac   835
Ala Val Glu His Phe Gly Asp Arg Phe Phe Glu Phe Arg Gln Gly Asn
230                 235                 240                 245

ctc ggc gga tcc ggc ggt tac tcc cgc atc atg ttc gaa gcc ctt ggc   883
Leu Gly Gly Ser Gly Gly Tyr Ser Arg Ile Met Phe Glu Ala Leu Gly
                250                 255                 260

gga gtc gac ggc aag ggc gaa gca ggc gct gcc aag agc cca tac atc   931
Gly Val Asp Gly Lys Gly Glu Ala Gly Ala Ala Lys Ser Pro Tyr Ile
            265                 270                 275

ctg tac atg gat gac gac att gct att gag cca gac tca gtg ctg cgt   979
Leu Tyr Met Asp Asp Asp Ile Ala Ile Glu Pro Asp Ser Val Leu Arg
        280                 285                 290

gcg ctt cag gta gcc cgc tac gca aaa tcc ccc atc ctc gtt ggc gga   1027
Ala Leu Gln Val Ala Arg Tyr Ala Lys Ser Pro Ile Leu Val Gly Gly
    295                 300                 305

caa atg ctc aac ctg caa gag cgc agc cac ctt cac acc atg ggc gaa   1075
Gln Met Leu Asn Leu Gln Glu Arg Ser His Leu His Thr Met Gly Glu
310                 315                 320                 325

gta gtt ggc gga cac gac ttc atg tgg acc gcc gca cca cac gtg cac   1123
Val Val Gly Gly His Asp Phe Met Trp Thr Ala Ala Pro His Val His
                330                 335                 340

tac gac cac gac ttc tct gca cac cca cta cat gat cgc ggt aaa ttc   1171
Tyr Asp His Asp Phe Ser Ala His Pro Leu His Asp Arg Gly Lys Phe
            345                 350                 355

gac gac aag cca gac gca cca aac tcc cgc gac ctg cac cgc cgc atc   1219
Asp Asp Lys Pro Asp Ala Pro Asn Ser Arg Asp Leu His Arg Arg Ile
        360                 365                 370

gac gtt gac ttc aac ggc tgg tgg atg tgc atg atc cca cgc gtt gtc   1267
Asp Val Asp Phe Asn Gly Trp Trp Met Cys Met Ile Pro Arg Val Val
    375                 380                 385

gcc gaa cag atc ggc caa cca ctc cca ctc ttt atc aag tgg gac gac   1315
Ala Glu Gln Ile Gly Gln Pro Leu Pro Leu Phe Ile Lys Trp Asp Asp
390                 395                 400                 405

gcc gaa tac ggt cta cgc gca cgc aaa gct gga ttc ccc aca gca acc   1363
Ala Glu Tyr Gly Leu Arg Ala Arg Lys Ala Gly Phe Pro Thr Ala Thr
                410                 415                 420

tgg cca gga atc gca atc tgg cac atg gcc tgg tcc gac aaa gac gac   1411
Trp Pro Gly Ile Ala Ile Trp His Met Ala Trp Ser Asp Lys Asp Asp
            425                 430                 435

gcc atc gac tgg cag gcc tac ttc cac ctc cgc aac cgc ctc gtg gtt   1459
Ala Ile Asp Trp Gln Ala Tyr Phe His Leu Arg Asn Arg Leu Val Val
        440                 445                 450

gcc gcg atg tac cac caa ggc agc gtc gac ggc att gtc cga tcg atg   1507
Ala Ala Met Tyr His Gln Gly Ser Val Asp Gly Ile Val Arg Ser Met
    455                 460                 465
```

```
caa aaa gcc acc ttc aag cac ctg ctg tgc ctg gaa tac tcc acc gtg   1555
Gln Lys Ala Thr Phe Lys His Leu Leu Cys Leu Glu Tyr Ser Thr Val
470                 475                 480                 485

gca atc caa aac gaa gca atg aag gac ttc ctt gca gga cca gat cag   1603
Ala Ile Gln Asn Glu Ala Met Lys Asp Phe Leu Ala Gly Pro Asp Gln
                490                 495                 500

ctc ttc tcg atc ctg gac acc tca cta cct cga att gca gcg att cgc   1651
Leu Phe Ser Ile Leu Asp Thr Ser Leu Pro Arg Ile Ala Ala Ile Arg
            505                 510                 515

aaa acc tat cca gac gcc gtt gtg ctg cca agc gcc acc gaa ctg cca   1699
Lys Thr Tyr Pro Asp Ala Val Val Leu Pro Ser Ala Thr Glu Leu Pro
        520                 525                 530

cga gca acc ggc gcg ccg ggt gtc cca acc aag gac atc ggt gga cgc   1747
Arg Ala Thr Gly Ala Pro Gly Val Pro Thr Lys Asp Ile Gly Gly Arg
    535                 540                 545

ctg gcc cca atc aag aag gca atg tgg ctg gct aag ggc ctg aag cac   1795
Leu Ala Pro Ile Lys Lys Ala Met Trp Leu Ala Lys Gly Leu Lys His
550                 555                 560                 565

tcc ctg tct aag gaa gat gcc tcc cac cac gag gtg cca cag gcc aac   1843
Ser Leu Ser Lys Glu Asp Ala Ser His His Glu Val Pro Gln Ala Asn
                570                 575                 580

ttc gca cca atc gaa gca cgt tgg ttc agc ctg tcc cga gtc gat ggc   1891
Phe Ala Pro Ile Glu Ala Arg Trp Phe Ser Leu Ser Arg Val Asp Gly
            585                 590                 595

gca aca gtt acc acc gcg gat ggc cgc ggc gtg gtc tac cgc aag cgc   1939
Ala Thr Val Thr Thr Ala Asp Gly Arg Gly Val Val Tyr Arg Lys Arg
        600                 605                 610

gac cgc gac aaa gct aaa gaa ctt ggc aaa gaa gca cgc gca ctg caa   1987
Asp Arg Asp Lys Ala Lys Glu Leu Gly Lys Glu Ala Arg Ala Leu Gln
    615                 620                 625

aag caa gta gca gag cgt ttc gac gaa ctc agt cgc gcc tac cgc aac   2035
Lys Gln Val Ala Glu Arg Phe Asp Glu Leu Ser Arg Ala Tyr Arg Asn
630                 635                 640                 645

gct cat cct gag ctt gtg agc cgt gaa gcc tgg gga aag gtc ttc gat   2083
Ala His Pro Glu Leu Val Ser Arg Glu Ala Trp Gly Lys Val Phe Asp
                650                 655                 660

gag caa taaggaagta cagattctgg tag                                2112
Glu Gln
```

<210> 2818
<211> 663
<212> PRT
<213> Corynebacterium glutamicum

<400> 2818

```
Met Lys Gly Glu Asp Thr Ser Met Ser Ala Thr Asn Leu Ala Val Glu
```

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  1               5                  10                  15

Gln Leu Gln Arg Val Leu Leu Pro Arg Arg Gly Glu Pro Ala Asp Val
            20                  25                  30

Arg Ser Leu Tyr Leu Leu Glu Ala Glu Ser Asn Lys Glu Arg Leu Glu
        35                  40                  45

Trp Glu Asp Arg Phe Ser Val Ser Val Pro Ala Gly Ala Glu Val Ser
    50                  55                  60

Phe Gln Thr Tyr Phe Asn Ala Phe Pro Ala Ser Tyr Trp Arg Arg Trp
65                  70                  75                  80

Ser Gln Leu Asp Ser Val Val Leu Lys Leu Lys Val Ser Gly Glu Ala
                85                  90                  95

Arg Val Asp Leu Tyr Arg Ser Lys Ile Asp Gly Ala Arg Ile Gly Ile
            100                 105                 110

Thr Gly Ser Val Val Lys Asp Asp Phe Ile Glu Phe Glu Val Ser Leu
        115                 120                 125

Ala Pro Phe Glu Asp Gly Gly Trp Ile Trp Phe Asp Leu Thr Ala Glu
    130                 135                 140

Thr Asp Ala Thr Val Glu Glu Ala Gly Trp Tyr Ala Pro His Ala Pro
145                 150                 155                 160

Lys Ala Gln Ile Met Pro Asp Gly Ser Glu Val Gly Pro Phe Glu Ala
                165                 170                 175

Arg Ala Thr Val Gly Ile Pro Thr Phe Asn Arg Pro Ala Asp Ala Val
            180                 185                 190

Ala Ala Leu Glu Ala Leu Ala Ser Asp Pro Ala Val Asp Ala Val Ile
        195                 200                 205

Asp Thr Val Ile Met Pro Asp Gln Gly Asn Lys His Pro Ala Asp Glu
    210                 215                 220

Pro Gly Tyr Lys Ala Ala Val Glu His Phe Gly Asp Arg Phe Phe Glu
225                 230                 235                 240

Phe Arg Gln Gly Asn Leu Gly Gly Ser Gly Gly Tyr Ser Arg Ile Met
                245                 250                 255

Phe Glu Ala Leu Gly Gly Val Asp Gly Lys Gly Glu Ala Gly Ala Ala
            260                 265                 270

Lys Ser Pro Tyr Ile Leu Tyr Met Asp Asp Asp Ile Ala Ile Glu Pro
        275                 280                 285

Asp Ser Val Leu Arg Ala Leu Gln Val Ala Arg Tyr Ala Lys Ser Pro
    290                 295                 300

Ile Leu Val Gly Gly Gln Met Leu Asn Leu Gln Glu Arg Ser His Leu
305                 310                 315                 320

His Thr Met Gly Glu Val Val Gly Gly His Asp Phe Met Trp Thr Ala
                325                 330                 335
```

```
Ala Pro His Val His Tyr Asp His Asp Phe Ser Ala His Pro Leu His
            340                 345                 350

Asp Arg Gly Lys Phe Asp Asp Lys Pro Asp Ala Pro Asn Ser Arg Asp
        355                 360                 365

Leu His Arg Arg Ile Asp Val Asp Phe Asn Gly Trp Trp Met Cys Met
    370                 375                 380

Ile Pro Arg Val Val Ala Glu Gln Ile Gly Gln Pro Leu Pro Leu Phe
385                 390                 395                 400

Ile Lys Trp Asp Asp Ala Glu Tyr Gly Leu Arg Ala Arg Lys Ala Gly
                405                 410                 415

Phe Pro Thr Ala Thr Trp Pro Gly Ile Ala Ile Trp His Met Ala Trp
            420                 425                 430

Ser Asp Lys Asp Asp Ala Ile Asp Trp Gln Ala Tyr Phe His Leu Arg
        435                 440                 445

Asn Arg Leu Val Val Ala Ala Met Tyr His Gln Gly Ser Val Asp Gly
    450                 455                 460

Ile Val Arg Ser Met Gln Lys Ala Thr Phe Lys His Leu Leu Cys Leu
465                 470                 475                 480

Glu Tyr Ser Thr Val Ala Ile Gln Asn Glu Ala Met Lys Asp Phe Leu
                485                 490                 495

Ala Gly Pro Asp Gln Leu Phe Ser Ile Leu Asp Thr Ser Leu Pro Arg
            500                 505                 510

Ile Ala Ala Ile Arg Lys Thr Tyr Pro Asp Ala Val Val Leu Pro Ser
        515                 520                 525

Ala Thr Glu Leu Pro Arg Ala Thr Gly Ala Pro Gly Val Pro Thr Lys
    530                 535                 540

Asp Ile Gly Gly Arg Leu Ala Pro Ile Lys Lys Ala Met Trp Leu Ala
545                 550                 555                 560

Lys Gly Leu Lys His Ser Leu Ser Lys Glu Asp Ala Ser His His Glu
                565                 570                 575

Val Pro Gln Ala Asn Phe Ala Pro Ile Glu Ala Arg Trp Phe Ser Leu
            580                 585                 590

Ser Arg Val Asp Gly Ala Thr Val Thr Thr Ala Asp Gly Arg Gly Val
        595                 600                 605

Val Tyr Arg Lys Arg Asp Arg Asp Lys Ala Lys Glu Leu Gly Lys Glu
    610                 615                 620

Ala Arg Ala Leu Gln Lys Gln Val Ala Glu Arg Phe Asp Glu Leu Ser
625                 630                 635                 640

Arg Ala Tyr Arg Asn Ala His Pro Glu Leu Val Ser Arg Glu Ala Trp
                645                 650                 655
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Gly Lys Val Phe Asp Glu Gln
            660


<210> 2819
<211> 627
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(604)
<223> RXA02602

<400> 2819
ctgcaaaagc aagtagcaga gcgtttcgac gaactcagtc gcgcctaccg caacgctcat 60

cctgagcttg tgagccgtga agcctgggga aaggtcttcg atg agc aat aag gaa   115
                                          Met Ser Asn Lys Glu
                                            1               5

gta cag att ctg gta gca atc cag gat caa ctc atg gat gcc cca gga   163
Val Gln Ile Leu Val Ala Ile Gln Asp Gln Leu Met Asp Ala Pro Gly
                 10                  15                  20

gta ctg ccc acc gca cga gga ctc agc ctg ctc ggc gaa cat gct gca   211
Val Leu Pro Thr Ala Arg Gly Leu Ser Leu Leu Gly Glu His Ala Ala
             25                  30                  35

ggc tgg ctg gca ctc ggc gct ggc ggt gct gtt gtg gac aaa aaa cgt   259
Gly Trp Leu Ala Leu Gly Ala Gly Gly Ala Val Val Asp Lys Lys Arg
         40                  45                  50

cgc cgc tcc tgg gct gga ctc ttc atc gct gca ctg gga agc cac gca   307
Arg Arg Ser Trp Ala Gly Leu Phe Ile Ala Ala Leu Gly Ser His Ala
     55                  60                  65

gca tca gtg atc atc aaa cga gtt gtc cgc cgc gct cgg cca cat gac   355
Ala Ser Val Ile Ile Lys Arg Val Val Arg Arg Ala Arg Pro His Asp
 70                  75                  80                  85

cca gcc atc agg att ggt gtg ggc acc ccc tca aag cta agc ttt cct   403
Pro Ala Ile Arg Ile Gly Val Gly Thr Pro Ser Lys Leu Ser Phe Pro
                 90                  95                 100

tct tca cat gcg acc tcg aca acc gca act atg gtt tat ctt gcg cgc   451
Ser Ser His Ala Thr Ser Thr Thr Ala Thr Met Val Tyr Leu Ala Arg
            105                 110                 115

atc acc aag tca cca gtg cca ctg cta gga atc ccc atc atg gtg cta   499
Ile Thr Lys Ser Pro Val Pro Leu Leu Gly Ile Pro Ile Met Val Leu
        120                 125                 130

tca cgc atg gtg ctt ggc gtg cat tac cca acc gat gtg cta gcc ggc   547
Ser Arg Met Val Leu Gly Val His Tyr Pro Thr Asp Val Leu Ala Gly
    135                 140                 145

gcg ttg ttg gga gca gcg acc gca gag gcc gtc cat aag atc gaa agg   595
Ala Leu Leu Gly Ala Ala Thr Ala Glu Ala Val His Lys Ile Glu Arg
150                 155                 160                 165
```

gct acg aag tgagcgaaca cgccgctgaa cat 627
Ala Thr Lys

<210> 2820
<211> 168
<212> PRT
<213> Corynebacterium glutamicum

<400> 2820
Met Ser Asn Lys Glu Val Gln Ile Leu Val Ala Ile Gln Asp Gln Leu
1 5 10 15

Met Asp Ala Pro Gly Val Leu Pro Thr Ala Arg Gly Leu Ser Leu Leu
20 25 30

Gly Glu His Ala Ala Gly Trp Leu Ala Leu Gly Ala Gly Gly Ala Val
35 40 45

Val Asp Lys Lys Arg Arg Arg Ser Trp Ala Gly Leu Phe Ile Ala Ala
50 55 60

Leu Gly Ser His Ala Ala Ser Val Ile Ile Lys Arg Val Val Arg Arg
65 70 75 80

Ala Arg Pro His Asp Pro Ala Ile Arg Ile Gly Val Gly Thr Pro Ser
85 90 95

Lys Leu Ser Phe Pro Ser Ser His Ala Thr Ser Thr Thr Ala Thr Met
100 105 110

Val Tyr Leu Ala Arg Ile Thr Lys Ser Pro Val Pro Leu Leu Gly Ile
115 120 125

Pro Ile Met Val Leu Ser Arg Met Val Leu Gly Val His Tyr Pro Thr
130 135 140

Asp Val Leu Ala Gly Ala Leu Leu Gly Ala Ala Thr Ala Glu Ala Val
145 150 155 160

His Lys Ile Glu Arg Ala Thr Lys
165

<210> 2821
<211> 2199
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2176)
<223> RXA02604

<400> 2821
tctgcatcgt gatggctgtg tacatcatgc cgatgttttg aatatttacc aatgaacatg 60

ctctgaccag catgtccatt aacgtttgag gccacatgcg gtg cta gca tgt ggc 115
Val Leu Ala Cys Gly
1 5

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ctc atg acg ttt agc ccc cag cgt ccg gag ttt gag acc ggt aag cag   163
Leu Met Thr Phe Ser Pro Gln Arg Pro Glu Phe Glu Thr Gly Lys Gln
                10                  15                  20

cca gat cca gaa act gaa cac gca ggt gac ttc ttt gaa gaa acc tca   211
Pro Asp Pro Glu Thr Glu His Ala Gly Asp Phe Phe Glu Glu Thr Ser
            25                  30                  35

agc agt gct cct cgc gcc gca tct aac ggt tct tct ggt ccg aac tac   259
Ser Ser Ala Pro Arg Ala Ala Ser Asn Gly Ser Ser Gly Pro Asn Tyr
        40                  45                  50

acc ctc att aca acg ttt cta gcg gcc ctt act gct ggc atc ttt gct   307
Thr Leu Ile Thr Thr Phe Leu Ala Ala Leu Thr Ala Gly Ile Phe Ala
    55                  60                  65

ttc tgg gca ggc tgg acc cgc aaa tgg atc agc gac gac gga ctg atc   355
Phe Trp Ala Gly Trp Thr Arg Lys Trp Ile Ser Asp Asp Gly Leu Ile
70                  75                  80                  85

gtc cta cgc acc gtc cga aac ctc ctg gct gga aac ggg cca gta ttc   403
Val Leu Arg Thr Val Arg Asn Leu Leu Ala Gly Asn Gly Pro Val Phe
                90                  95                  100

aac gct ggc gaa cgc gtc gaa gcc aac aca tct act ctg tgg caa tac   451
Asn Ala Gly Glu Arg Val Glu Ala Asn Thr Ser Thr Leu Trp Gln Tyr
            105                 110                 115

tgc atc tat ctg gtt gcc tta gta act gac tat cgc ctc gaa gat att   499
Cys Ile Tyr Leu Val Ala Leu Val Thr Asp Tyr Arg Leu Glu Asp Ile
        120                 125                 130

gct ctg tgg ctt gcg ctg ctg ttc acc acc gca gcg tcc atc atc ggt   547
Ala Leu Trp Leu Ala Leu Leu Phe Thr Thr Ala Ala Ser Ile Ile Gly
    135                 140                 145

gtc ctg ggt acc gcg cat ctc cac cgc aaa cgc att gcc gta ttg ctt   595
Val Leu Gly Thr Ala His Leu His Arg Lys Arg Ile Ala Val Leu Leu
150                 155                 160                 165

cct gca ggc gtg atc ggc tac ttc agc ctt tcc ccg gcg cga gac ttt   643
Pro Ala Gly Val Ile Gly Tyr Phe Ser Leu Ser Pro Ala Arg Asp Phe
                170                 175                 180

gcc act tcc gga ttg gag tgg ggc cta tct ttg atg tgg att tcc atc   691
Ala Thr Ser Gly Leu Glu Trp Gly Leu Ser Leu Met Trp Ile Ser Ile
            185                 190                 195

caa tgg ctg ctg ctg gtg ttg tgg gcg act tcg ggc aag acc tcg ggc   739
Gln Trp Leu Leu Leu Val Leu Trp Ala Thr Ser Gly Lys Thr Ser Gly
        200                 205                 210

aag aag gct tcg ggc gca aaa act tca aat cct atc gtt aat gcc ggt   787
Lys Lys Ala Ser Gly Ala Lys Thr Ser Asn Pro Ile Val Asn Ala Gly
    215                 220                 225

gca ata acc tat gct ttg gcc ttt tgg tca ggc ttg agc tgg ctg gtt   835
Ala Ile Thr Tyr Ala Leu Ala Phe Trp Ser Gly Leu Ser Trp Leu Val
230                 235                 240                 245
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cgc cca gaa ctg gcg atg tat ggc ggt ttg act gga gtg ttg ctg ctg   883
Arg Pro Glu Leu Ala Met Tyr Gly Gly Leu Thr Gly Val Leu Leu Leu
                250                 255                 260

ctt act gcg cca cga tgg cgg gta gtt ttg ggg atc ctg gtg gcg gct   931
Leu Thr Ala Pro Arg Trp Arg Val Val Leu Gly Ile Leu Val Ala Ala
            265                 270                 275

ttg cct ctt cca gct gcg tac caa atc ttc cgc atg ggt tat tac ggg   979
Leu Pro Leu Pro Ala Ala Tyr Gln Ile Phe Arg Met Gly Tyr Tyr Gly
        280                 285                 290

ctg atg gtg ccg cac acg gct gta gcg aaa tca gcc tca gat gcg gtg   1027
Leu Met Val Pro His Thr Ala Val Ala Lys Ser Ala Ser Asp Ala Val
    295                 300                 305

tgg ggg act ggt tgg gaa tat gtt gag gat ttc acg ggg cct tac aac   1075
Trp Gly Thr Gly Trp Glu Tyr Val Glu Asp Phe Thr Gly Pro Tyr Asn
310                 315                 320                 325

ctg tgg ctc ggt ttg gcc ttg ctg ttg gcc gca ggc gcg ttg aca gtg   1123
Leu Trp Leu Gly Leu Ala Leu Leu Leu Ala Ala Gly Ala Leu Thr Val
                330                 335                 340

tgg aaa act gac aag cac tta gcg ata ccg aag ggg cgg ctg ggg ctg   1171
Trp Lys Thr Asp Lys His Leu Ala Ile Pro Lys Gly Arg Leu Gly Leu
            345                 350                 355

cgc act ccg ggt atg gct ata gcg ttg ctg gtt atc tgt gcg ctc gtc   1219
Arg Thr Pro Gly Met Ala Ile Ala Leu Leu Val Ile Cys Ala Leu Val
        360                 365                 370

cac ttc ctt tac gtt atc cgt gtt ggt ggc gac ttc atg cat gga cgc   1267
His Phe Leu Tyr Val Ile Arg Val Gly Gly Asp Phe Met His Gly Arg
    375                 380                 385

atg ctg ctc ctt cca ctt ttt gcc att ctg ctg cct gtt tct gtc att   1315
Met Leu Leu Leu Pro Leu Phe Ala Ile Leu Leu Pro Val Ser Val Ile
390                 395                 400                 405

ccg gtc aat gtt gtt gat cga ggt tgg cag gat ttg gtt gcg ctg gtt   1363
Pro Val Asn Val Val Asp Arg Gly Trp Gln Asp Leu Val Ala Leu Val
                410                 415                 420

ctc gtt ttc tct acg tgg gtg tgg tcc act gtg gtt ttt gtg cag ggg   1411
Leu Val Phe Ser Thr Trp Val Trp Ser Thr Val Val Phe Val Gln Gly
            425                 430                 435

cac caa tgg gaa aat acc ggc cag cat gtg gtt gat gag cgt gat ttt   1459
His Gln Trp Glu Asn Thr Gly Gln His Val Val Asp Glu Arg Asp Phe
        440                 445                 450

tgg att gat ttc acc aac cga gat gaa gat cat cct ccg ctt tat gca   1507
Trp Ile Asp Phe Thr Asn Arg Asp Glu Asp His Pro Pro Leu Tyr Ala
    455                 460                 465

gag gat ttc ctc act gtt gat tcc atg aat gat tac gca gag gtt atg   1555
Glu Asp Phe Leu Thr Val Asp Ser Met Asn Asp Tyr Ala Glu Val Met
470                 475                 480                 485

cgc gat cag acg ttg gtt aat cca aca ggc cag caa ctc aat att ctg   1603
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Arg Asp Gln Thr Leu Val Asn Pro Thr Gly Gln Gln Leu Asn Ile Leu
                490                 495                 500

gcc agc agt gac ccg acc act tat tcg tgg atc acc aca cct cgc gtg   1651
Ala Ser Ser Asp Pro Thr Thr Tyr Ser Trp Ile Thr Thr Pro Arg Val
            505                 510                 515

gag ggg gtt gaa gcc ggt gat ttg gct aac ctc tcg cca act gtt ttc   1699
Glu Gly Val Glu Ala Gly Asp Leu Ala Asn Leu Ser Pro Thr Val Phe
        520                 525                 530

cat gtg aac ctc ggc atg acc tcc atg aac gca ccg ctc aac gtg cgt   1747
His Val Asn Leu Gly Met Thr Ser Met Asn Ala Pro Leu Asn Val Arg
    535                 540                 545

gtg aca gac ctg att ggt ttg gca acg cca ctg gca gcc cgc cag cca   1795
Val Thr Asp Leu Ile Gly Leu Ala Thr Pro Leu Ala Ala Arg Gln Pro
550                 555                 560                 565

cgc att gaa ggt ggt cga atc ggc cac gat aaa ttg atg gac ttg gaa   1843
Arg Ile Glu Gly Gly Arg Ile Gly His Asp Lys Leu Met Asp Leu Glu
                570                 575                 580

tgg cag gtc gcg gaa tcc gcc act ccg ctg gcg tac aca ccg ggt tgg   1891
Trp Gln Val Ala Glu Ser Ala Thr Pro Leu Ala Tyr Thr Pro Gly Trp
            585                 590                 595

ttg gat act caa aag act tat gag gcc cgc cag gcg cta cgc cac cca   1939
Leu Asp Thr Gln Lys Thr Tyr Glu Ala Arg Gln Ala Leu Arg His Pro
        600                 605                 610

gaa ttg gtt cac ctt ttc cag act tac cgt gag cca atg tcc tac cac   1987
Glu Leu Val His Leu Phe Gln Thr Tyr Arg Glu Pro Met Ser Tyr His
    615                 620                 625

cgg ttt gtg gac aat att aaa tac gca ctc act acc gga aga aca ctg   2035
Arg Phe Val Asp Asn Ile Lys Tyr Ala Leu Thr Thr Gly Arg Thr Leu
630                 635                 640                 645

gaa att tca gat aat cct gaa gat ctt ttg aaa gaa ttt aac ccg acc   2083
Glu Ile Ser Asp Asn Pro Glu Asp Leu Leu Lys Glu Phe Asn Pro Thr
                650                 655                 660

cct gca gag att cag gac ggg tta gaa act att gct tgg cct ggg gaa   2131
Pro Ala Glu Ile Gln Asp Gly Leu Glu Thr Ile Ala Trp Pro Gly Glu
            665                 670                 675

att aaa ctt gat gaa cct cgc gga gaa cct tta tat agc tct cag       2176
Ile Lys Leu Asp Glu Pro Arg Gly Glu Pro Leu Tyr Ser Ser Gln
        680                 685                 690

taaacactta ttcgcaaatc att                                        2199


<210> 2822
<211> 692
<212> PRT
<213> Corynebacterium glutamicum

<400> 2822
Val Leu Ala Cys Gly Leu Met Thr Phe Ser Pro Gln Arg Pro Glu Phe
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  1               5                  10                  15
Glu Thr Gly Lys Gln Pro Asp Pro Glu Thr Glu His Ala Gly Asp Phe
            20                  25                  30
Phe Glu Glu Thr Ser Ser Ser Ala Pro Arg Ala Ala Ser Asn Gly Ser
        35                  40                  45
Ser Gly Pro Asn Tyr Thr Leu Ile Thr Thr Phe Leu Ala Ala Leu Thr
    50                  55                  60
Ala Gly Ile Phe Ala Phe Trp Ala Gly Trp Thr Arg Lys Trp Ile Ser
65                  70                  75                  80
Asp Asp Gly Leu Ile Val Leu Arg Thr Val Arg Asn Leu Leu Ala Gly
                85                  90                  95
Asn Gly Pro Val Phe Asn Ala Gly Glu Arg Val Glu Ala Asn Thr Ser
            100                 105                 110
Thr Leu Trp Gln Tyr Cys Ile Tyr Leu Val Ala Leu Val Thr Asp Tyr
        115                 120                 125
Arg Leu Glu Asp Ile Ala Leu Trp Leu Ala Leu Leu Phe Thr Thr Ala
    130                 135                 140
Ala Ser Ile Ile Gly Val Leu Gly Thr Ala His Leu His Arg Lys Arg
145                 150                 155                 160
Ile Ala Val Leu Leu Pro Ala Gly Val Ile Gly Tyr Phe Ser Leu Ser
                165                 170                 175
Pro Ala Arg Asp Phe Ala Thr Ser Gly Leu Glu Trp Gly Leu Ser Leu
            180                 185                 190
Met Trp Ile Ser Ile Gln Trp Leu Leu Leu Val Leu Trp Ala Thr Ser
        195                 200                 205
Gly Lys Thr Ser Gly Lys Lys Ala Ser Gly Ala Lys Thr Ser Asn Pro
    210                 215                 220
Ile Val Asn Ala Gly Ala Ile Thr Tyr Ala Leu Ala Phe Trp Ser Gly
225                 230                 235                 240
Leu Ser Trp Leu Val Arg Pro Glu Leu Ala Met Tyr Gly Gly Leu Thr
                245                 250                 255
Gly Val Leu Leu Leu Leu Thr Ala Pro Arg Trp Arg Val Val Leu Gly
            260                 265                 270
Ile Leu Val Ala Ala Leu Pro Leu Pro Ala Ala Tyr Gln Ile Phe Arg
        275                 280                 285
Met Gly Tyr Tyr Gly Leu Met Val Pro His Thr Ala Val Ala Lys Ser
    290                 295                 300
Ala Ser Asp Ala Val Trp Gly Thr Gly Trp Glu Tyr Val Glu Asp Phe
305                 310                 315                 320
Thr Gly Pro Tyr Asn Leu Trp Leu Gly Leu Ala Leu Leu Leu Ala Ala
                325                 330                 335
```

Gly Ala Leu Thr Val Trp Lys Thr Asp Lys His Leu Ala Ile Pro Lys
340 345 350

Gly Arg Leu Gly Leu Arg Thr Pro Gly Met Ala Ile Ala Leu Leu Val
355 360 365

Ile Cys Ala Leu Val His Phe Leu Tyr Val Ile Arg Val Gly Gly Asp
370 375 380

Phe Met His Gly Arg Met Leu Leu Leu Pro Leu Phe Ala Ile Leu Leu
385 390 395 400

Pro Val Ser Val Ile Pro Val Asn Val Val Asp Arg Gly Trp Gln Asp
405 410 415

Leu Val Ala Leu Val Leu Val Phe Ser Thr Trp Val Trp Ser Thr Val
420 425 430

Val Phe Val Gln Gly His Gln Trp Glu Asn Thr Gly Gln His Val Val
435 440 445

Asp Glu Arg Asp Phe Trp Ile Asp Phe Thr Asn Arg Asp Glu Asp His
450 455 460

Pro Pro Leu Tyr Ala Glu Asp Phe Leu Thr Val Asp Ser Met Asn Asp
465 470 475 480

Tyr Ala Glu Val Met Arg Asp Gln Thr Leu Val Asn Pro Thr Gly Gln
485 490 495

Gln Leu Asn Ile Leu Ala Ser Ser Asp Pro Thr Thr Tyr Ser Trp Ile
500 505 510

Thr Thr Pro Arg Val Glu Gly Val Glu Ala Gly Asp Leu Ala Asn Leu
515 520 525

Ser Pro Thr Val Phe His Val Asn Leu Gly Met Thr Ser Met Asn Ala
530 535 540

Pro Leu Asn Val Arg Val Thr Asp Leu Ile Gly Leu Ala Thr Pro Leu
545 550 555 560

Ala Ala Arg Gln Pro Arg Ile Glu Gly Gly Arg Ile Gly His Asp Lys
565 570 575

Leu Met Asp Leu Glu Trp Gln Val Ala Glu Ser Ala Thr Pro Leu Ala
580 585 590

Tyr Thr Pro Gly Trp Leu Asp Thr Gln Lys Thr Tyr Glu Ala Arg Gln
595 600 605

Ala Leu Arg His Pro Glu Leu Val His Leu Phe Gln Thr Tyr Arg Glu
610 615 620

Pro Met Ser Tyr His Arg Phe Val Asp Asn Ile Lys Tyr Ala Leu Thr
625 630 635 640

Thr Gly Arg Thr Leu Glu Ile Ser Asp Asn Pro Glu Asp Leu Leu Lys
645 650 655

```
Glu Phe Asn Pro Thr Pro Ala Glu Ile Gln Asp Gly Leu Glu Thr Ile
            660                 665                 670

Ala Trp Pro Gly Glu Ile Lys Leu Asp Glu Pro Arg Gly Glu Pro Leu
        675                 680                 685

Tyr Ser Ser Gln
    690


<210> 2823
<211> 372
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(349)
<223> RXA02609

<400> 2823
gaccgaacgc agcagtcagg cgtcgcaaag caatggaagc ggcggaagca cagcccggga 60

cggggcagcc gaggaaatcg acggcctgcc cgaggtgacc gtg gaa cgc agc gct   115
                                              Val Glu Arg Ser Ala
                                                1               5

gag gcg caa gcg ttc ctg gat gcg ctg aaa gat gaa aaa atc gac atc   163
Glu Ala Gln Ala Phe Leu Asp Ala Leu Lys Asp Glu Lys Ile Asp Ile
                10                  15                  20

tcc ggc gtg gag gac cag ttg att gcg act gcg cga aat tac tgc agt   211
Ser Gly Val Glu Asp Gln Leu Ile Ala Thr Ala Arg Asn Tyr Cys Ser
            25                  30                  35

tcg gaa aac aag gac caa aac gtc act gtc gat gcg gtt gca ggc cag   259
Ser Glu Asn Lys Asp Gln Asn Val Thr Val Asp Ala Val Ala Gly Gln
        40                  45                  50

ctc atc gtg cag gga cgc acc agc gtg aag gaa gat caa gca gcg gaa   307
Leu Ile Val Gln Gly Arg Thr Ser Val Lys Glu Asp Gln Ala Ala Glu
    55                  60                  65

att tct acg ctg ctg aag gaa tct gcg gat cgg acg tat tgt           349
Ile Ser Thr Leu Leu Lys Glu Ser Ala Asp Arg Thr Tyr Cys
70                  75                  80

taaccgatga ggaaaaccat cac                                        372


<210> 2824
<211> 83
<212> PRT
<213> Corynebacterium glutamicum

<400> 2824
Val Glu Arg Ser Ala Glu Ala Gln Ala Phe Leu Asp Ala Leu Lys Asp
  1               5                  10                  15

Glu Lys Ile Asp Ile Ser Gly Val Glu Asp Gln Leu Ile Ala Thr Ala
            20                  25                  30
```

```
Arg Asn Tyr Cys Ser Ser Glu Asn Lys Asp Gln Asn Val Thr Val Asp
         35                  40                  45

Ala Val Ala Gly Gln Leu Ile Val Gln Gly Arg Thr Ser Val Lys Glu
     50                  55                  60

Asp Gln Ala Ala Glu Ile Ser Thr Leu Leu Lys Glu Ser Ala Asp Arg
 65                  70                  75                  80

Thr Tyr Cys
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<210> 2825
<211> 630
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(607)
<223> RXA02617

<400> 2825

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ctctttaatt aacttttggg cgacccttta cggtcgtcct cttgcgttcc caaaacatac 60

ccagtaagtt actgggtatc caactcttga ttggggaaca atg tcc ata aaa cat   115
                                            Met Ser Ile Lys His
                                              1               5

gca ctc ttg gtg ctc atg ctc gac gaa cca acc tcg gca agt cag ctg   163
Ala Leu Leu Val Leu Met Leu Asp Glu Pro Thr Ser Ala Ser Gln Leu
                 10                  15                  20

caa acc aag ttt gaa gaa aca atg ggg atc tgg cag ctc aat atc ggc   211
Gln Thr Lys Phe Glu Glu Thr Met Gly Ile Trp Gln Leu Asn Ile Gly
             25                  30                  35

caa gtc acc caa acc atc cag cgg cta cag cgc gac ggc ctg gcg gaa   259
Gln Val Thr Gln Thr Ile Gln Arg Leu Gln Arg Asp Gly Leu Ala Glu
         40                  45                  50

acc gca ggc acc acc gtc agt tcc aac ggc cgc acc gta gat act ttc   307
Thr Ala Gly Thr Thr Val Ser Ser Asn Gly Arg Thr Val Asp Thr Phe
     55                  60                  65

cag ccc acg gac tta ggt cgc gaa ctt gtc gcg cag tgg ttc gaa agt   355
Gln Pro Thr Asp Leu Gly Arg Glu Leu Val Ala Gln Trp Phe Glu Ser
 70                  75                  80                  85

ccc gtc acc gtc aca ctg tcc gaa cgc gat gaa tta gtc acc aaa atc   403
Pro Val Thr Val Thr Leu Ser Glu Arg Asp Glu Leu Val Thr Lys Ile
                 90                  95                 100

gcc atc gca gaa tca cgt ggc ctc aat ttg att cca ctt tta gac att   451
Ala Ile Ala Glu Ser Arg Gly Leu Asn Leu Ile Pro Leu Leu Asp Ile
             105                 110                 115

caa cgc aac aca gtc atg gcg gaa cta cgc gca ctc aac aaa tcc agc   499
Gln Arg Asn Thr Val Met Ala Glu Leu Arg Ala Leu Asn Lys Ser Ser
```

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        120                 125                 130

cgc gat ctc gcc gaa acc aga aac acc cag cgg ctc ctc gtc gaa aag   547
Arg Asp Leu Ala Glu Thr Arg Asn Thr Gln Arg Leu Leu Val Glu Lys
    135                 140                 145

cga atc ttt gaa cta gaa gcc cag gca cgt tgg ctc gac cga att gaa   595
Arg Ile Phe Glu Leu Glu Ala Gln Ala Arg Trp Leu Asp Arg Ile Glu
150                 155                 160                 165

gca ttg gag cag taaatgacaa acacgccttt ccc                        630
Ala Leu Glu Gln
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<210> 2826
<211> 169
<212> PRT
<213> Corynebacterium glutamicum

<400> 2826

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Met Ser Ile Lys His Ala Leu Leu Val Leu Met Leu Asp Glu Pro Thr
  1               5                  10                  15

Ser Ala Ser Gln Leu Gln Thr Lys Phe Glu Glu Thr Met Gly Ile Trp
             20                  25                  30

Gln Leu Asn Ile Gly Gln Val Thr Gln Thr Ile Gln Arg Leu Gln Arg
         35                  40                  45

Asp Gly Leu Ala Glu Thr Ala Gly Thr Thr Val Ser Ser Asn Gly Arg
     50                  55                  60

Thr Val Asp Thr Phe Gln Pro Thr Asp Leu Gly Arg Glu Leu Val Ala
 65                  70                  75                  80

Gln Trp Phe Glu Ser Pro Val Thr Val Thr Leu Ser Glu Arg Asp Glu
                 85                  90                  95

Leu Val Thr Lys Ile Ala Ile Ala Glu Ser Arg Gly Leu Asn Leu Ile
            100                 105                 110

Pro Leu Leu Asp Ile Gln Arg Asn Thr Val Met Ala Glu Leu Arg Ala
        115                 120                 125

Leu Asn Lys Ser Ser Arg Asp Leu Ala Glu Thr Arg Asn Thr Gln Arg
    130                 135                 140

Leu Leu Val Glu Lys Arg Ile Phe Glu Leu Glu Ala Gln Ala Arg Trp
145                 150                 155                 160

Leu Asp Arg Ile Glu Ala Leu Glu Gln
                165
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<210> 2827
<211> 1023
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS
<222> (101)..(1000)
<223> RXA02619

<400> 2827
agcgacttct caaagaacca ccccactcat ttcgagtgcg ggtggttttt tctatgccta 60

attctatgcc taattctatg tctgattcta ttggtgtcgc atg cgc agt gta gtt 115
Met Arg Ser Val Val
1 5

tta gaa cta cta gag aac tgg aag gaa tca ctc gtg ctt cac ccc tca 163
Leu Glu Leu Leu Glu Asn Trp Lys Glu Ser Leu Val Leu His Pro Ser
10 15 20

ttg act gag cta gcg gat gct gcc cca ctt gca cag gat ttt gcc acc 211
Leu Thr Glu Leu Ala Asp Ala Ala Pro Leu Ala Gln Asp Phe Ala Thr
25 30 35

gtc cgc ggt gtg ctg aag gaa tcg ctg gat ttg ttg ggc aat gca ctg 259
Val Arg Gly Val Leu Lys Glu Ser Leu Asp Leu Leu Gly Asn Ala Leu
40 45 50

aac cac ggt gaa gag ccc gcg gag ctt gca ggg tgg ctg tca caa gtt 307
Asn His Gly Glu Glu Pro Ala Glu Leu Ala Gly Trp Leu Ser Gln Val
55 60 65

att act gat gtt ttg cac tcc cct ggc ttg gat gcc cac gtg gtg ctc 355
Ile Thr Asp Val Leu His Ser Pro Gly Leu Asp Ala His Val Val Leu
70 75 80 85

acc ggc ccc gtg ggg cgt gga gac gca ctg cct acc tcg ccc gtg agg 403
Thr Gly Pro Val Gly Arg Gly Asp Ala Leu Pro Thr Ser Pro Val Arg
90 95 100

tgg ctg gcg gtc gtc gat agc caa gaa gat ccg aat gaa aag att tca 451
Trp Leu Ala Val Val Asp Ser Gln Glu Asp Pro Asn Glu Lys Ile Ser
105 110 115

gcg ctg tta act gag gtg ggc ttc att gcg gag ccg atc ggt gcg gca 499
Ala Leu Leu Thr Glu Val Gly Phe Ile Ala Glu Pro Ile Gly Ala Ala
120 125 130

act cgt gag gag tgg gag cag cgt gcg cgc gct ggt gag gat cca gag 547
Thr Arg Glu Glu Trp Glu Gln Arg Ala Arg Ala Gly Glu Asp Pro Glu
135 140 145

gtc tat ttg gat gct ggc acg tgg gtc gcg gcg atc gct gaa gta gat 595
Val Tyr Leu Asp Ala Gly Thr Trp Val Ala Ala Ile Ala Glu Val Asp
150 155 160 165

gac aaa gca ctg ttg cag gat gcg ttg tca tct agg ccg cct gcg gtg 643
Asp Lys Ala Leu Leu Gln Asp Ala Leu Ser Ser Arg Pro Pro Ala Val
170 175 180

gaa act tat gag ggt ctt cct tcg ttg gac atg gtg gta aac att cgt 691
Glu Thr Tyr Glu Gly Leu Pro Ser Leu Asp Met Val Val Asn Ile Arg
185 190 195

gag aac ctc atg att ccc acg gtg aag atc gct cgc tgg gca gca cac 739
Glu Asn Leu Met Ile Pro Thr Val Lys Ile Ala Arg Trp Ala Ala His

```
        200                 205                 210

aag gct ggt tct ttg gcg cct acg act gcg cag cgc ctc gtg gat gcc   787
Lys Ala Gly Ser Leu Ala Pro Thr Thr Ala Gln Arg Leu Val Asp Ala
    215                 220                 225

cgt ggt gtg ctc acc aat gat gaa gtc gac gcg ctg aca cag gtg tgg   835
Arg Gly Val Leu Thr Asn Asp Glu Val Asp Ala Leu Thr Gln Val Trp
230                 235                 240                 245

act tcc gca ctg agc ttg cag tcg aaa cgt tgg atg gat cac atc cat   883
Thr Ser Ala Leu Ser Leu Gln Ser Lys Arg Trp Met Asp His Ile His
                250                 255                 260

gat caa gaa acc acc gct tgg gag ctt ccc gcg ctg caa cgt gcc act   931
Asp Gln Glu Thr Thr Ala Trp Glu Leu Pro Ala Leu Gln Arg Ala Thr
            265                 270                 275

ttt ggc gca tcg gct cgg ttg ctt tct gag gtg ttg cgg tcc gtt gaa   979
Phe Gly Ala Ser Ala Arg Leu Leu Ser Glu Val Leu Arg Ser Val Glu
        280                 285                 290

gcc cgt gaa atc gat acc aaa taggaactct gcacaattac tgg            1023
Ala Arg Glu Ile Asp Thr Lys
    295                 300
```

Sequence Listing

<210> 2828
<211> 300
<212> PRT
<213> Corynebacterium glutamicum

<400> 2828

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Met Arg Ser Val Val Leu Glu Leu Leu Glu Asn Trp Lys Glu Ser Leu
  1               5                  10                  15

Val Leu His Pro Ser Leu Thr Glu Leu Ala Asp Ala Ala Pro Leu Ala
             20                  25                  30

Gln Asp Phe Ala Thr Val Arg Gly Val Leu Lys Glu Ser Leu Asp Leu
         35                  40                  45

Leu Gly Asn Ala Leu Asn His Gly Glu Glu Pro Ala Glu Leu Ala Gly
     50                  55                  60

Trp Leu Ser Gln Val Ile Thr Asp Val Leu His Ser Pro Gly Leu Asp
 65                  70                  75                  80

Ala His Val Val Leu Thr Gly Pro Val Gly Arg Gly Asp Ala Leu Pro
                 85                  90                  95

Thr Ser Pro Val Arg Trp Leu Ala Val Val Asp Ser Gln Glu Asp Pro
            100                 105                 110

Asn Glu Lys Ile Ser Ala Leu Leu Thr Glu Val Gly Phe Ile Ala Glu
        115                 120                 125

Pro Ile Gly Ala Ala Thr Arg Glu Glu Trp Glu Gln Arg Ala Arg Ala
    130                 135                 140

Gly Glu Asp Pro Glu Val Tyr Leu Asp Ala Gly Thr Trp Val Ala Ala
```

```
145                 150                 155                 160

Ile Ala Glu Val Asp Asp Lys Ala Leu Leu Gln Asp Ala Leu Ser Ser
                165                 170                 175

Arg Pro Pro Ala Val Glu Thr Tyr Glu Gly Leu Pro Ser Leu Asp Met
            180                 185                 190

Val Val Asn Ile Arg Glu Asn Leu Met Ile Pro Thr Val Lys Ile Ala
        195                 200                 205

Arg Trp Ala Ala His Lys Ala Gly Ser Leu Ala Pro Thr Thr Ala Gln
    210                 215                 220

Arg Leu Val Asp Ala Arg Gly Val Leu Thr Asn Asp Glu Val Asp Ala
225                 230                 235                 240

Leu Thr Gln Val Trp Thr Ser Ala Leu Ser Leu Gln Ser Lys Arg Trp
                245                 250                 255

Met Asp His Ile His Asp Gln Glu Thr Thr Ala Trp Glu Leu Pro Ala
            260                 265                 270

Leu Gln Arg Ala Thr Phe Gly Ala Ser Ala Arg Leu Leu Ser Glu Val
        275                 280                 285

Leu Arg Ser Val Glu Ala Arg Glu Ile Asp Thr Lys
    290                 295                 300


<210> 2829
<211> 777
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(754)
<223> RXA02620

<400> 2829
atcgatacca aataggaact ctgcacaatt actggctaca atctcttgag atcaataggc 60

caaaacttta aggaagtaga attacgctat ggcaggagca gtg gga cgc ccc cgg   115
                                               Val Gly Arg Pro Arg
                                                 1               5

aga tca gct ccg cga cgg gca ggc aag aat cct cgc gag gag att ctt   163
Arg Ser Ala Pro Arg Arg Ala Gly Lys Asn Pro Arg Glu Glu Ile Leu
                10                  15                  20

gac gcc tct gct gag ctt ttc acc cgt caa ggc ttc gca aca acc tcc   211
Asp Ala Ser Ala Glu Leu Phe Thr Arg Gln Gly Phe Ala Thr Thr Ser
            25                  30                  35

acg cat caa atc gct gat gcc gtg gga atc cgc caa gcc tcg ctg tat   259
Thr His Gln Ile Ala Asp Ala Val Gly Ile Arg Gln Ala Ser Leu Tyr
        40                  45                  50

tat cac ttc ccg tcc aag acg gaa atc ttc ctc acc ctg ctg aaa tct   307
Tyr His Phe Pro Ser Lys Thr Glu Ile Phe Leu Thr Leu Leu Lys Ser
```

```
     55                  60                  65

act gtc gag ccg tcc act gtg ctc gcc gaa gac tta agc acc ctg gac   355
Thr Val Glu Pro Ser Thr Val Leu Ala Glu Asp Leu Ser Thr Leu Asp
 70                  75                  80                  85

gcc gga cct gag atg cgc ctc tgg gca atc gtt gcc tcc gaa gtg cgt   403
Ala Gly Pro Glu Met Arg Leu Trp Ala Ile Val Ala Ser Glu Val Arg
                90                  95                 100

ctg ctg ctg tcc acc aag tgg aac gtc ggt cgc ctg tac caa ctc ccc   451
Leu Leu Leu Ser Thr Lys Trp Asn Val Gly Arg Leu Tyr Gln Leu Pro
            105                 110                 115

atc gtt ggt tct gaa gag ttc gcc gag tac cac agc cag cgc gaa gcc   499
Ile Val Gly Ser Glu Glu Phe Ala Glu Tyr His Ser Gln Arg Glu Ala
        120                 125                 130

ctc acc aac gtc ttc cgc gac ctc gcc acc gaa atc gtc ggt gac gac   547
Leu Thr Asn Val Phe Arg Asp Leu Ala Thr Glu Ile Val Gly Asp Asp
    135                 140                 145

ccc cgc gca gaa ctc ccc ttc cac atc acc atg tcg gtg atc gaa atg   595
Pro Arg Ala Glu Leu Pro Phe His Ile Thr Met Ser Val Ile Glu Met
150                 155                 160                 165

cgt cgc aac gac ggc aag att cca agc ccg ctt tcc gca gac agc ctc   643
Arg Arg Asn Asp Gly Lys Ile Pro Ser Pro Leu Ser Ala Asp Ser Leu
                170                 175                 180

ccg gag acc gca att atg ctt gcc gac gcc tcc ctc gcc gtc ctc ggc   691
Pro Glu Thr Ala Ile Met Leu Ala Asp Ala Ser Leu Ala Val Leu Gly
            185                 190                 195

gcg ccg ctg ccc gcc gac cgg gtc gaa aaa acg ctt gaa cta atc aag   739
Ala Pro Leu Pro Ala Asp Arg Val Glu Lys Thr Leu Glu Leu Ile Lys
        200                 205                 210

cag gct gac gcg aaa taaccatccg cgcctgcgaa atc                     777
Gln Ala Asp Ala Lys
    215
```

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Sequence Listing - Page 3230 of 3230

<210> 2830
<211> 218
<212> PRT
<213> Corynebacterium glutamicum

<400> 2830

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Val Gly Arg Pro Arg Arg Ser Ala Pro Arg Arg Ala Gly Lys Asn Pro
  1               5                  10                  15

Arg Glu Glu Ile Leu Asp Ala Ser Ala Glu Leu Phe Thr Arg Gln Gly
             20                  25                  30

Phe Ala Thr Thr Ser Thr His Gln Ile Ala Asp Ala Val Gly Ile Arg
         35                  40                  45

Gln Ala Ser Leu Tyr Tyr His Phe Pro Ser Lys Thr Glu Ile Phe Leu
     50                  55                  60
```

```
Thr Leu Leu Lys Ser Thr Val Glu Pro Ser Thr Val Leu Ala Glu Asp
 65                  70                  75                  80

Leu Ser Thr Leu Asp Ala Gly Pro Glu Met Arg Leu Trp Ala Ile Val
                85                  90                  95

Ala Ser Glu Val Arg Leu Leu Leu Ser Thr Lys Trp Asn Val Gly Arg
            100                 105                 110

Leu Tyr Gln Leu Pro Ile Val Gly Ser Glu Glu Phe Ala Glu Tyr His
        115                 120                 125

Ser Gln Arg Glu Ala Leu Thr Asn Val Phe Arg Asp Leu Ala Thr Glu
    130                 135                 140

Ile Val Gly Asp Asp Pro Arg Ala Glu Leu Pro Phe His Ile Thr Met
145                 150                 155                 160

Ser Val Ile Glu Met Arg Arg Asn Asp Gly Lys Ile Pro Ser Pro Leu
                165                 170                 175

Ser Ala Asp Ser Leu Pro Glu Thr Ala Ile Met Leu Ala Asp Ala Ser
            180                 185                 190

Leu Ala Val Leu Gly Ala Pro Leu Pro Ala Asp Arg Val Glu Lys Thr
        195                 200                 205

Leu Glu Leu Ile Lys Gln Ala Asp Ala Lys
    210                 215


<210> 2831
<211> 957
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(934)
<223> RXA02639

<400> 2831
cgaaaatgtt ggaaatcgcc gaacgggaac gtcgacaagc aaaacgcgcg gcaaaggtcg 60

ccaagaaacg caccaccttt ataaggaaaa tctttaaaaa atg att gca ctg ggt   115
                                            Met Ile Ala Leu Gly
                                              1               5

tca gcg ccc aag ctg gtt gcc tcc gat gtt gat ggc acc ctc atc aat   163
Ser Ala Pro Lys Leu Val Ala Ser Asp Val Asp Gly Thr Leu Ile Asn
                10                  15                  20

agt tct gag cgc gtg ccg caa cgc ctg cgc gat gtg atc acg cgg atg   211
Ser Ser Glu Arg Val Pro Gln Arg Leu Arg Asp Val Ile Thr Arg Met
            25                  30                  35

acc aat cag ggc gtg acc ctg gcg ctg tcc acg ggc cgc ccg ccg cgc   259
Thr Asn Gln Gly Val Thr Leu Ala Leu Ser Thr Gly Arg Pro Pro Arg
        40                  45                  50

tgg att cat tat gtg ctg gat cag ctg agc gtg aag ccg att tgc gtc   307
```

```
Trp Ile His Tyr Val Leu Asp Gln Leu Ser Val Lys Pro Ile Cys Val
     55                  60                  65

tgc gcg aat ggc gcg gtg ctg tac gat tcc gct gcc gat gag att ctt   355
Cys Ala Asn Gly Ala Val Leu Tyr Asp Ser Ala Ala Asp Glu Ile Leu
 70                  75                  80                  85

gca gct cag acg ctt agt ccg gag gtt atg gcg agt gcc gtc atg gct   403
Ala Ala Gln Thr Leu Ser Pro Glu Val Met Ala Ser Ala Val Met Ala
                90                  95                 100

gcg cgt gcc gct ttg gaa gag cat ggc ggg gtc agt att gct gtc gag   451
Ala Arg Ala Ala Leu Glu Glu His Gly Gly Val Ser Ile Ala Val Glu
            105                 110                 115

cgc gct gga aaa tcc gct tac gat cca gcc gat gag ctg ttt ttg gtc   499
Arg Ala Gly Lys Ser Ala Tyr Asp Pro Ala Asp Glu Leu Phe Leu Val
        120                 125                 130

acc ccg gaa tac agc cac gcg tgg ccc tca aat gat cac ggc acc ttc   547
Thr Pro Glu Tyr Ser His Ala Trp Pro Ser Asn Asp His Gly Thr Phe
    135                 140                 145

gag gaa gcc gaa gtg ctt tcc gaa cca gcc acc aaa ttg ttg atg cgc   595
Glu Glu Ala Glu Val Leu Ser Glu Pro Ala Thr Lys Leu Leu Met Arg
150                 155                 160                 165

agc gat tac ctc gat tcc aag cag ctt ttt gat atc gtc cgc gcc tcc   643
Ser Asp Tyr Leu Asp Ser Lys Gln Leu Phe Asp Ile Val Arg Ala Ser
                170                 175                 180

gtt ccc gag gat caa gtc cac gtc acc ttc tcc atg tcc ggc gga ctc   691
Val Pro Glu Asp Gln Val His Val Thr Phe Ser Met Ser Gly Gly Leu
            185                 190                 195

att gag atc gca gcg ccc ggc gtg acc aag gca ctg ggc gta tcg atg   739
Ile Glu Ile Ala Ala Pro Gly Val Thr Lys Ala Leu Gly Val Ser Met
        200                 205                 210

ctg gca gag cgc cta aag att gcg caa aag gac gtt ata acg ttc ggc   787
Leu Ala Glu Arg Leu Lys Ile Ala Gln Lys Asp Val Ile Thr Phe Gly
    215                 220                 225

gac atg ccc aac gat att gaa atg ctc cag tgg gcc ggc cgg gga gtg   835
Asp Met Pro Asn Asp Ile Glu Met Leu Gln Trp Ala Gly Arg Gly Val
230                 235                 240                 245

gcg atg ggc aac gcc cga cca gag gtc aaa gcc gtg tca gac cac atc   883
Ala Met Gly Asn Ala Arg Pro Glu Val Lys Ala Val Ser Asp His Ile
                250                 255                 260

acc cgc acc aac gac gac gcc ggt gta gca gat gta ttg gag tgg tgg   931
Thr Arg Thr Asn Asp Asp Ala Gly Val Ala Asp Val Leu Glu Trp Trp
            265                 270                 275

ttc taataggtgg tgttaaaaca ctg                                    957
Phe
```

<210> 2832

<211> 278
<212> PRT
<213> Corynebacterium glutamicum

<400> 2832

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Met Ile Ala Leu Gly Ser Ala Pro Lys Leu Val Ala Ser Asp Val Asp
  1               5                  10                  15

Gly Thr Leu Ile Asn Ser Ser Glu Arg Val Pro Gln Arg Leu Arg Asp
             20                  25                  30

Val Ile Thr Arg Met Thr Asn Gln Gly Val Thr Leu Ala Leu Ser Thr
         35                  40                  45

Gly Arg Pro Pro Arg Trp Ile His Tyr Val Leu Asp Gln Leu Ser Val
     50                  55                  60

Lys Pro Ile Cys Val Cys Ala Asn Gly Ala Val Leu Tyr Asp Ser Ala
 65                  70                  75                  80

Ala Asp Glu Ile Leu Ala Ala Gln Thr Leu Ser Pro Glu Val Met Ala
                 85                  90                  95

Ser Ala Val Met Ala Ala Arg Ala Ala Leu Glu Glu His Gly Gly Val
            100                 105                 110

Ser Ile Ala Val Glu Arg Ala Gly Lys Ser Ala Tyr Asp Pro Ala Asp
        115                 120                 125

Glu Leu Phe Leu Val Thr Pro Glu Tyr Ser His Ala Trp Pro Ser Asn
    130                 135                 140

Asp His Gly Thr Phe Glu Glu Ala Glu Val Leu Ser Glu Pro Ala Thr
145                 150                 155                 160

Lys Leu Leu Met Arg Ser Asp Tyr Leu Asp Ser Lys Gln Leu Phe Asp
                165                 170                 175

Ile Val Arg Ala Ser Val Pro Glu Asp Gln Val His Val Thr Phe Ser
            180                 185                 190

Met Ser Gly Gly Leu Ile Glu Ile Ala Ala Pro Gly Val Thr Lys Ala
        195                 200                 205

Leu Gly Val Ser Met Leu Ala Glu Arg Leu Lys Ile Ala Gln Lys Asp
    210                 215                 220

Val Ile Thr Phe Gly Asp Met Pro Asn Asp Ile Glu Met Leu Gln Trp
225                 230                 235                 240

Ala Gly Arg Gly Val Ala Met Gly Asn Ala Arg Pro Glu Val Lys Ala
                245                 250                 255

Val Ser Asp His Ile Thr Arg Thr Asn Asp Asp Ala Gly Val Ala Asp
            260                 265                 270

Val Leu Glu Trp Trp Phe
        275
```

<210> 2833

<211> 585
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(562)
<223> RXA02647

<400> 2833
atcttctatc ttgtttccat agtaaatccg catatttatt gccaggagaa aagttttgtc 60

tttgcgtcga agtactttga cccttgttac agcaagcgct gtg gca ttg tcc gtg 115
Val Ala Leu Ser Val
1 5

ttc act cca gtt gcc cag gct cag tcc tct gac gca ctg aca cag ctc 163
Phe Thr Pro Val Ala Gln Ala Gln Ser Ser Asp Ala Leu Thr Gln Leu
10 15 20

tca gac aac atc acc tca tca cag atc ctt gat gat gat gga aat cca 211
Ser Asp Asn Ile Thr Ser Ser Gln Ile Leu Asp Asp Asp Gly Asn Pro
25 30 35

gtc gat gga aac gaa acc tgg cca ggc agc tct gaa ggc agc tca atg 259
Val Asp Gly Asn Glu Thr Trp Pro Gly Ser Ser Glu Gly Ser Ser Met
40 45 50

ctc agc aat ggc gac att cct gcg gcc cca agc ttg agc tcc tcc ggc 307
Leu Ser Asn Gly Asp Ile Pro Ala Ala Pro Ser Leu Ser Ser Ser Gly
55 60 65

aaa gac acc agc gat gat gac gat gaa atc agc gaa gag cag caa gca 355
Lys Asp Thr Ser Asp Asp Asp Asp Glu Ile Ser Glu Glu Gln Gln Ala
70 75 80 85

ctg atc gat cgg ttg tcc gaa atg cca gtg att ggt tcc att gtc tcc 403
Leu Ile Asp Arg Leu Ser Glu Met Pro Val Ile Gly Ser Ile Val Ser
90 95 100

cca cca gaa tgg ctt gcc att cct ttt gcg gta ctg cag gga ttg ctc 451
Pro Pro Glu Trp Leu Ala Ile Pro Phe Ala Val Leu Gln Gly Leu Leu
105 110 115

gca atc acc act ctt gct tcc acc gca gca tcc ttc atg gtg acc gtc 499
Ala Ile Thr Thr Leu Ala Ser Thr Ala Ala Ser Phe Met Val Thr Val
120 125 130

gac cca tcg ttc aag cag act ctg cgt gac atg ctc acc cag ttt ggc 547
Asp Pro Ser Phe Lys Gln Thr Leu Arg Asp Met Leu Thr Gln Phe Gly
135 140 145

atc aac gtc gac gct taaaagcaca ctgacataaa atg 585
Ile Asn Val Asp Ala
150

<210> 2834
<211> 154
<212> PRT
<213> Corynebacterium glutamicum

<400> 2834
Val Ala Leu Ser Val Phe Thr Pro Val Ala Gln Ala Gln Ser Ser Asp
1 5 10 15

Ala Leu Thr Gln Leu Ser Asp Asn Ile Thr Ser Ser Gln Ile Leu Asp
20 25 30

Asp Asp Gly Asn Pro Val Asp Gly Asn Glu Thr Trp Pro Gly Ser Ser
35 40 45

Glu Gly Ser Ser Met Leu Ser Asn Gly Asp Ile Pro Ala Ala Pro Ser
50 55 60

Leu Ser Ser Ser Gly Lys Asp Thr Ser Asp Asp Asp Asp Glu Ile Ser
65 70 75 80

Glu Glu Gln Gln Ala Leu Ile Asp Arg Leu Ser Glu Met Pro Val Ile
85 90 95

Gly Ser Ile Val Ser Pro Pro Glu Trp Leu Ala Ile Pro Phe Ala Val
100 105 110

Leu Gln Gly Leu Leu Ala Ile Thr Thr Leu Ala Ser Thr Ala Ala Ser
115 120 125

Phe Met Val Thr Val Asp Pro Ser Phe Lys Gln Thr Leu Arg Asp Met
130 135 140

Leu Thr Gln Phe Gly Ile Asn Val Asp Ala
145 150

<210> 2835
<211> 1125
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1102)
<223> RXA02649

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ttttacacag ttgcagcaaa aattcggcca ttccgattgc ttttgacagc taaactttgc 60

atttgttctt tttggcgccg atgccgatag gtttaaaggc gtg cta aaa cga ttc 115
Val Leu Lys Arg Phe
1 5

tct cac cac tcc agc ccg caa gtt ctt tca cgg aaa gtt gtc gcg tcc 163
Ser His His Ser Ser Pro Gln Val Leu Ser Arg Lys Val Val Ala Ser
10 15 20

gca tta gct tta aca acc gcg ctg gct tta gcc gcg tgt agt tcc tca 211
Ala Leu Ala Leu Thr Thr Ala Leu Ala Leu Ala Ala Cys Ser Ser Ser
25 30 35

gcc gag ccg gac tcc cct gaa gtt gag cag gcg gtg ggt ctt gcg gtg 259
Ala Glu Pro Asp Ser Pro Glu Val Glu Gln Ala Val Gly Leu Ala Val
40 45 50

```
gat acg cca cgt gtg gtg gtt gtg gat cca ggc act ggc gat ttg cag   307
Asp Thr Pro Arg Val Val Val Val Asp Pro Gly Thr Gly Asp Leu Gln
     55                  60                  65

cgc ttg caa tac aaa gac atc gcc cct gat gcc aca cag gaa cag acc   355
Arg Leu Gln Tyr Lys Asp Ile Ala Pro Asp Ala Thr Gln Glu Gln Thr
 70                  75                  80                  85

atc aat att gct gaa ggt ttt gcc caa tcg gtg gtg aat gcg gac agc   403
Ile Asn Ile Ala Glu Gly Phe Ala Gln Ser Val Val Asn Ala Asp Ser
                90                  95                 100

gtg gat ccg cag gca cca gcc ggt ggc gat gtc acc aca ttc cac ctt   451
Val Asp Pro Gln Ala Pro Ala Gly Gly Asp Val Thr Thr Phe His Leu
            105                 110                 115

cct gtt aaa gcc acc acc gag gaa gcg gag ttc agc gat cag gaa atg   499
Pro Val Lys Ala Thr Thr Glu Glu Ala Glu Phe Ser Asp Gln Glu Met
        120                 125                 130

gtg agc gcg act cgc gat atc tct cta ctt ttc ggt aaa cct acc tac   547
Val Ser Ala Thr Arg Asp Ile Ser Leu Leu Phe Gly Lys Pro Thr Tyr
    135                 140                 145

acc gat ctt tcc caa gtt gaa gat gtg aat tcc acc gag gga ttc acg   595
Thr Asp Leu Ser Gln Val Glu Asp Val Asn Ser Thr Glu Gly Phe Thr
150                 155                 160                 165

ctg gga atc cgc gca aca gat agt gga cag cac acc acc tta agt ttc   643
Leu Gly Ile Arg Ala Thr Asp Ser Gly Gln His Thr Thr Leu Ser Phe
                170                 175                 180

gca gcc cct gtt gat tcc act gaa act ggt cgc atg ctc atg gag caa   691
Ala Ala Pro Val Asp Ser Thr Glu Thr Gly Arg Met Leu Met Glu Gln
            185                 190                 195

tac tta ctc acg ttt acg tcc ctt ccc att gtg ttc ccc tct gac gat   739
Tyr Leu Leu Thr Phe Thr Ser Leu Pro Ile Val Phe Pro Ser Asp Asp
        200                 205                 210

att ggc gtg ggc gcg aag tgg act gtg gat agc cgt gtg aca ggc gaa   787
Ile Gly Val Gly Ala Lys Trp Thr Val Asp Ser Arg Val Thr Gly Glu
    215                 220                 225

tca acg ctg cta caa acc gtg acc tac acg atc aca ggg atc gac ggc   835
Ser Thr Leu Leu Gln Thr Val Thr Tyr Thr Ile Thr Gly Ile Asp Gly
230                 235                 240                 245

gac aaa gta aac ctc gat gtg gaa gtc tct cag cgc ccc agc atg ggt   883
Asp Lys Val Asn Leu Asp Val Glu Val Ser Gln Arg Pro Ser Met Gly
                250                 255                 260

gcg ttg gag atc acc gat gaa gaa tcg gac gag acc acc ggg cag ctc   931
Ala Leu Glu Ile Thr Asp Glu Glu Ser Asp Glu Thr Thr Gly Gln Leu
            265                 270                 275

act gtc ctt aat tcc aac acc acc tcc gtg ggc acc ttg gaa gtc gat   979
Thr Val Leu Asn Ser Asn Thr Thr Ser Val Gly Thr Leu Glu Val Asp
        280                 285                 290
```

```
ctg act cag cct tta ccc acg tca gga cag gtt tct tgg acc act cgc   1027
Leu Thr Gln Pro Leu Pro Thr Ser Gly Gln Val Ser Trp Thr Thr Arg
    295                 300                 305

gtg att tac ggc ggt tcc aat gag cag gtg cgt gtg gtg cag gat tcc   1075
Val Ile Tyr Gly Gly Ser Asn Glu Gln Val Arg Val Val Gln Asp Ser
310                 315                 320                 325

acc tct tcg gtg agc ttc gga gac cag taatttacca attagggttg         1122
Thr Ser Ser Val Ser Phe Gly Asp Gln
                330

cca                                                               1125
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<210> 2836
<211> 334
<212> PRT
<213> Corynebacterium glutamicum

<400> 2836

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Val Leu Lys Arg Phe Ser His His Ser Ser Pro Gln Val Leu Ser Arg
  1               5                  10                  15

Lys Val Val Ala Ser Ala Leu Ala Leu Thr Thr Ala Leu Ala Leu Ala
             20                  25                  30

Ala Cys Ser Ser Ser Ala Glu Pro Asp Ser Pro Glu Val Glu Gln Ala
         35                  40                  45

Val Gly Leu Ala Val Asp Thr Pro Arg Val Val Val Val Asp Pro Gly
     50                  55                  60

Thr Gly Asp Leu Gln Arg Leu Gln Tyr Lys Asp Ile Ala Pro Asp Ala
 65                  70                  75                  80

Thr Gln Glu Gln Thr Ile Asn Ile Ala Glu Gly Phe Ala Gln Ser Val
                 85                  90                  95

Val Asn Ala Asp Ser Val Asp Pro Gln Ala Pro Ala Gly Gly Asp Val
            100                 105                 110

Thr Thr Phe His Leu Pro Val Lys Ala Thr Thr Glu Glu Ala Glu Phe
        115                 120                 125

Ser Asp Gln Glu Met Val Ser Ala Thr Arg Asp Ile Ser Leu Leu Phe
    130                 135                 140

Gly Lys Pro Thr Tyr Thr Asp Leu Ser Gln Val Glu Asp Val Asn Ser
145                 150                 155                 160

Thr Glu Gly Phe Thr Leu Gly Ile Arg Ala Thr Asp Ser Gly Gln His
                165                 170                 175

Thr Thr Leu Ser Phe Ala Ala Pro Val Asp Ser Thr Glu Thr Gly Arg
            180                 185                 190

Met Leu Met Glu Gln Tyr Leu Leu Thr Phe Thr Ser Leu Pro Ile Val
        195                 200                 205

Phe Pro Ser Asp Asp Ile Gly Val Gly Ala Lys Trp Thr Val Asp Ser
```

```
    210                 215                 220

Arg Val Thr Gly Glu Ser Thr Leu Leu Gln Thr Val Thr Tyr Thr Ile
225                 230                 235                 240

Thr Gly Ile Asp Gly Asp Lys Val Asn Leu Asp Val Glu Val Ser Gln
                245                 250                 255

Arg Pro Ser Met Gly Ala Leu Glu Ile Thr Asp Glu Glu Ser Asp Glu
            260                 265                 270

Thr Thr Gly Gln Leu Thr Val Leu Asn Ser Asn Thr Thr Ser Val Gly
        275                 280                 285

Thr Leu Glu Val Asp Leu Thr Gln Pro Leu Pro Thr Ser Gly Gln Val
    290                 295                 300

Ser Trp Thr Thr Arg Val Ile Tyr Gly Gly Ser Asn Glu Gln Val Arg
305                 310                 315                 320

Val Val Gln Asp Ser Thr Ser Ser Val Ser Phe Gly Asp Gln
                325                 330
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<210> 2837
<211> 702
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(679)
<223> RXA02652

<400> 2837

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cgcttggatt caaccaccca gcagatggcc gatggatgga aatcgtctcc ccatatccaa 60

ctgatctcca acacgcttta gacgttctcc gcgagcaata atg gat ggt gtc gat   115
                                              Met Asp Gly Val Asp
                                                1               5

aaa ggg cga cgc atc gtc gcc ctc cta gca att ctc gca ttg gtt gtc   163
Lys Gly Arg Arg Ile Val Ala Leu Leu Ala Ile Leu Ala Leu Val Val
                 10                  15                  20

gtg gtt gcg atc ttg agt ttc agc gac cgc acc gcg aaa ccc atg cag   211
Val Val Ala Ile Leu Ser Phe Ser Asp Arg Thr Ala Lys Pro Met Gln
             25                  30                  35

ctc aac ggt gac atg ctc ggc caa gac aac acg gaa act tcc gtc gag   259
Leu Asn Gly Asp Met Leu Gly Gln Asp Asn Thr Glu Thr Ser Val Glu
         40                  45                  50

tac cgt cag cgg gca tcg gaa tca ttg gaa aat gcc gcg gtc ggc gaa   307
Tyr Arg Gln Arg Ala Ser Glu Ser Leu Glu Asn Ala Ala Val Gly Glu
     55                  60                  65

gaa gcc tat tca ctg gtg acg ttc aca cag ccg ctt tcg cct tcc gag   355
Glu Ala Tyr Ser Leu Val Thr Phe Thr Gln Pro Leu Ser Pro Ser Glu
 70                  75                  80                  85
```

```
gcc tct aac ctt ctt aaa gga gtc ggt cgc gtc aat gcc atg gtt atg   403
Ala Ser Asn Leu Leu Lys Gly Val Gly Arg Val Asn Ala Met Val Met
                 90                  95                 100

ctc tcg gct cct gcc atg gat cta ccc gaa ccc atc gca ggc gag acc   451
Leu Ser Ala Pro Ala Met Asp Leu Pro Glu Pro Ile Ala Gly Glu Thr
            105                 110                 115

cgt gaa gat gtt ttt aac cgt caa ata aag ctt gtc gac gcc cag tta   499
Arg Glu Asp Val Phe Asn Arg Gln Ile Lys Leu Val Asp Ala Gln Leu
        120                 125                 130

tcc ggt atc ggc aac gtc cgc gcg ccg ggc gaa ctc aac ggg gta gtg   547
Ser Gly Ile Gly Asn Val Arg Ala Pro Gly Glu Leu Asn Gly Val Val
    135                 140                 145

gtt tgg gat att cct cag aaa gtt cgt gtg ttg tcc gag agc tcg ctg   595
Val Trp Asp Ile Pro Gln Lys Val Arg Val Leu Ser Glu Ser Ser Leu
150                 155                 160                 165

gtt tat agt gtc gaa acc ctg cca cct gac gcg gcg tgg ggc agt ttc   643
Val Tyr Ser Val Glu Thr Leu Pro Pro Asp Ala Ala Trp Gly Ser Phe
                170                 175                 180

ggt att cga cca gtc gat act tcg ggt act aat ttt tagaagaaaa        689
Gly Ile Arg Pro Val Asp Thr Ser Gly Thr Asn Phe
            185                 190

ttccagatgc ccc                                                   702
```

<210> 2838
<211> 193
<212> PRT
<213> Corynebacterium glutamicum

<400> 2838

```
Met Asp Gly Val Asp Lys Gly Arg Arg Ile Val Ala Leu Leu Ala Ile
  1               5                  10                  15

Leu Ala Leu Val Val Val Val Ala Ile Leu Ser Phe Ser Asp Arg Thr
             20                  25                  30

Ala Lys Pro Met Gln Leu Asn Gly Asp Met Leu Gly Gln Asp Asn Thr
         35                  40                  45

Glu Thr Ser Val Glu Tyr Arg Gln Arg Ala Ser Glu Ser Leu Glu Asn
     50                  55                  60

Ala Ala Val Gly Glu Glu Ala Tyr Ser Leu Val Thr Phe Thr Gln Pro
 65                  70                  75                  80

Leu Ser Pro Ser Glu Ala Ser Asn Leu Leu Lys Gly Val Gly Arg Val
                 85                  90                  95

Asn Ala Met Val Met Leu Ser Ala Pro Ala Met Asp Leu Pro Glu Pro
            100                 105                 110

Ile Ala Gly Glu Thr Arg Glu Asp Val Phe Asn Arg Gln Ile Lys Leu
        115                 120                 125
```

```
Val Asp Ala Gln Leu Ser Gly Ile Gly Asn Val Arg Ala Pro Gly Glu
    130                 135                 140

Leu Asn Gly Val Val Val Trp Asp Ile Pro Gln Lys Val Arg Val Leu
145                 150                 155                 160

Ser Glu Ser Ser Leu Val Tyr Ser Val Glu Thr Leu Pro Pro Asp Ala
                165                 170                 175

Ala Trp Gly Ser Phe Gly Ile Arg Pro Val Asp Thr Ser Gly Thr Asn
            180                 185                 190

Phe
```

<210> 2839
<211> 1107
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1084)
<223> RXA02655

<400> 2839

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aattcgatgg agaagaaaaa gtcatggggg tcaggctagg agaaaatgat ctcatgatgg 60

ctttggaacg gtacctcgct cacgagtttg gtgaaattag atg agt cca gaa gcc   115
                                              Met Ser Pro Glu Ala
                                                1               5

aaa gaa gcc caa gat tct agg cgc aac gag atg ccc gag aaa aag cga   163
Lys Glu Ala Gln Asp Ser Arg Arg Asn Glu Met Pro Glu Lys Lys Arg
                10                  15                  20

gcg gtg cta cgt aaa gcg att aag ttg gaa tgg gca acg atc gca tgg   211
Ala Val Leu Arg Lys Ala Ile Lys Leu Glu Trp Ala Thr Ile Ala Trp
            25                  30                  35

gtt ctt ttt tcg atc gtt ttg gta ggt gtt gtc gct ggt caa tcg cag   259
Val Leu Phe Ser Ile Val Leu Val Gly Val Val Ala Gly Gln Ser Gln
        40                  45                  50

gcc atg cgt agt gca tgg att gaa gac atg ctt tct ttg gta cca cct   307
Ala Met Arg Ser Ala Trp Ile Glu Asp Met Leu Ser Leu Val Pro Pro
    55                  60                  65

atc gct ttt ctt tta gcc tcc cga atc agc aaa gct gtg gca acc aga   355
Ile Ala Phe Leu Leu Ala Ser Arg Ile Ser Lys Ala Val Ala Thr Arg
70                  75                  80                  85

aaa cat cca tac ggc aag cac cgg tcg att gct atc ggg cac caa gct   403
Lys His Pro Tyr Gly Lys His Arg Ser Ile Ala Ile Gly His Gln Ala
                90                  95                  100

gca gca ctg gcc ctg ctt atc atg gga agc ctt tta att tat gaa gcg   451
Ala Ala Leu Ala Leu Leu Ile Met Gly Ser Leu Leu Ile Tyr Glu Ala
            105                 110                 115
```

```
gta tct gca ctg atc aag gga gaa agg cct ccg ata ggt tta gct att   499
Val Ser Ala Leu Ile Lys Gly Glu Arg Pro Pro Ile Gly Leu Ala Ile
        120                 125                 130

tta ttt ggc cat gac gtg tgg tca ggt tgg tta atg atc ggg gtt atg   547
Leu Phe Gly His Asp Val Trp Ser Gly Trp Leu Met Ile Gly Val Met
    135                 140                 145

att tca gtg tcg atc ccg atg gtg att gta ggg cga gta aaa ata aac   595
Ile Ser Val Ser Ile Pro Met Val Ile Val Gly Arg Val Lys Ile Asn
150                 155                 160                 165

tta gct aaa gat ctc cac gat aaa ctc ctc tat gca gac gcg gat atg   643
Leu Ala Lys Asp Leu His Asp Lys Leu Leu Tyr Ala Asp Ala Asp Met
                170                 175                 180

gcc aag gct gac tgg ggc aca gca gtc gct agc aca gta ggc gtg ctc   691
Ala Lys Ala Asp Trp Gly Thr Ala Val Ala Ser Thr Val Gly Val Leu
            185                 190                 195

gga ata gga ctg ggt ttt tgg tgg gcg gat gca gtt gca gct cta gta   739
Gly Ile Gly Leu Gly Phe Trp Trp Ala Asp Ala Val Ala Ala Leu Val
        200                 205                 210

ata tca gct tca att ctc aga gat ggc gtg ata aat atg aaa gct gct   787
Ile Ser Ala Ser Ile Leu Arg Asp Gly Val Ile Asn Met Lys Ala Ala
    215                 220                 225

ata tct gac tta ggt gat gga cga gcc atg act tat gac aat tcc gcc   835
Ile Ser Asp Leu Gly Asp Gly Arg Ala Met Thr Tyr Asp Asn Ser Ala
230                 235                 240                 245

cct cac cca tta aat gat gat gtg gaa aag gct gcc cta gag atg cat   883
Pro His Pro Leu Asn Asp Asp Val Glu Lys Ala Ala Leu Glu Met His
                250                 255                 260

tgg gtc aaa cac gcc cgc gct agg ata cgc gac caa ggc cgc tgt ttc   931
Trp Val Lys His Ala Arg Ala Arg Ile Arg Asp Gln Gly Arg Cys Phe
            265                 270                 275

cac aca gag tta ttt gtc gaa cca gta gaa gga tac aca cct gct ccg   979
His Thr Glu Leu Phe Val Glu Pro Val Glu Gly Tyr Thr Pro Ala Pro
        280                 285                 290

gaa gaa ata act tct cta gtt aag cga atc caa aac ctt gac tgg aag   1027
Glu Glu Ile Thr Ser Leu Val Lys Arg Ile Gln Asn Leu Asp Trp Lys
    295                 300                 305

ctg caa gat gtc gta gct tcc gtc gtc gaa aaa atc gac cgg ttt cag   1075
Leu Gln Asp Val Val Ala Ser Val Val Glu Lys Ile Asp Arg Phe Gln
310                 315                 320                 325

gcc cct tcg taaaacttaa ctgagaaagt gat                            1107
Ala Pro Ser
```

<210> 2840
<211> 328
<212> PRT
<213> Corynebacterium glutamicum

<400> 2840

```
Met Ser Pro Glu Ala Lys Glu Ala Gln Asp Ser Arg Arg Asn Glu Met
  1               5                  10                  15

Pro Glu Lys Lys Arg Ala Val Leu Arg Lys Ala Ile Lys Leu Glu Trp
             20                  25                  30

Ala Thr Ile Ala Trp Val Leu Phe Ser Ile Val Leu Val Gly Val Val
         35                  40                  45

Ala Gly Gln Ser Gln Ala Met Arg Ser Ala Trp Ile Glu Asp Met Leu
     50                  55                  60

Ser Leu Val Pro Pro Ile Ala Phe Leu Leu Ala Ser Arg Ile Ser Lys
 65                  70                  75                  80

Ala Val Ala Thr Arg Lys His Pro Tyr Gly Lys His Arg Ser Ile Ala
                 85                  90                  95

Ile Gly His Gln Ala Ala Ala Leu Ala Leu Leu Ile Met Gly Ser Leu
            100                 105                 110

Leu Ile Tyr Glu Ala Val Ser Ala Leu Ile Lys Gly Glu Arg Pro Pro
        115                 120                 125

Ile Gly Leu Ala Ile Leu Phe Gly His Asp Val Trp Ser Gly Trp Leu
    130                 135                 140

Met Ile Gly Val Met Ile Ser Val Ser Ile Pro Met Val Ile Val Gly
145                 150                 155                 160

Arg Val Lys Ile Asn Leu Ala Lys Asp Leu His Asp Lys Leu Leu Tyr
                165                 170                 175

Ala Asp Ala Asp Met Ala Lys Ala Asp Trp Gly Thr Ala Val Ala Ser
            180                 185                 190

Thr Val Gly Val Leu Gly Ile Gly Leu Gly Phe Trp Trp Ala Asp Ala
        195                 200                 205

Val Ala Ala Leu Val Ile Ser Ala Ser Ile Leu Arg Asp Gly Val Ile
    210                 215                 220

Asn Met Lys Ala Ala Ile Ser Asp Leu Gly Asp Gly Arg Ala Met Thr
225                 230                 235                 240

Tyr Asp Asn Ser Ala Pro His Pro Leu Asn Asp Asp Val Glu Lys Ala
                245                 250                 255

Ala Leu Glu Met His Trp Val Lys His Ala Arg Ala Arg Ile Arg Asp
            260                 265                 270

Gln Gly Arg Cys Phe His Thr Glu Leu Phe Val Glu Pro Val Glu Gly
        275                 280                 285

Tyr Thr Pro Ala Pro Glu Glu Ile Thr Ser Leu Val Lys Arg Ile Gln
    290                 295                 300

Asn Leu Asp Trp Lys Leu Gln Asp Val Val Ala Ser Val Val Glu Lys
305                 310                 315                 320
```

```
Ile Asp Arg Phe Gln Ala Pro Ser
                325


<210> 2841
<211> 387
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(364)
<223> RXA02662

<400> 2841
ccaaggtgtc accctcaccg ttgccatcgc cttcatcatc gtcaatatcg ccgtggacct 60

gctctacgtc ctggtcaatc cacgtattag gagcatctag atg cgc cgt aaa cta   115
                                            Met Arg Arg Lys Leu
                                              1               5

acc acc aca tta gaa aac aag ccc ggt gca cga ctt ggt ggc ttc cgc   163
Thr Thr Thr Leu Glu Asn Lys Pro Gly Ala Arg Leu Gly Gly Phe Arg
                 10                  15                  20

gca ctt gca cca act tca aaa atc gcg ctg gtt ttc ctt ctc ctg atc   211
Ala Leu Ala Pro Thr Ser Lys Ile Ala Leu Val Phe Leu Leu Leu Ile
             25                  30                  35

ttc ctc ctc gcg atc ttt gcc cca ctg att gct aaa tac gat cca ctg   259
Phe Leu Leu Ala Ile Phe Ala Pro Leu Ile Ala Lys Tyr Asp Pro Leu
         40                  45                  50

gcc tcc gga act cca gtc cag cct cca agc ggt gag cac tgg ttt ggt   307
Ala Ser Gly Thr Pro Val Gln Pro Pro Ser Gly Glu His Trp Phe Gly
     55                  60                  65

acc gac gcc atc ggc cgc gat att ttc tcc cgc gta gcc acg gcg cca   355
Thr Asp Ala Ile Gly Arg Asp Ile Phe Ser Arg Val Ala Thr Ala Pro
 70                  75                  80                  85

gag cct ccc tgatcattgg tcttttcgct acg                            387
Glu Pro Pro


<210> 2842
<211> 88
<212> PRT
<213> Corynebacterium glutamicum

<400> 2842
Met Arg Arg Lys Leu Thr Thr Thr Leu Glu Asn Lys Pro Gly Ala Arg
  1               5                  10                  15

Leu Gly Gly Phe Arg Ala Leu Ala Pro Thr Ser Lys Ile Ala Leu Val
             20                  25                  30

Phe Leu Leu Leu Ile Phe Leu Leu Ala Ile Phe Ala Pro Leu Ile Ala
         35                  40                  45
```

```
Lys Tyr Asp Pro Leu Ala Ser Gly Thr Pro Val Gln Pro Pro Ser Gly
     50                  55                  60

Glu His Trp Phe Gly Thr Asp Ala Ile Gly Arg Asp Ile Phe Ser Arg
 65                  70                  75                  80

Val Ala Thr Ala Pro Glu Pro Pro
                 85


<210> 2843
<211> 603
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(580)
<223> RXA02665

<400> 2843
caaggcgacc caatggcgtt taaagtaaca acccccattg atatgatgct ggcacaacgc 60

atcaccgacg aagccgaacc cacaatattt gaggtaccag gtg act aac cca atc   115
                                            Val Thr Asn Pro Ile
                                              1               5

atc ccc cgc gta gga atc gcc aca gac gcc cac caa atc gaa gcg gga   163
Ile Pro Arg Val Gly Ile Ala Thr Asp Ala His Gln Ile Glu Ala Gly
                10                  15                  20

aaa ccc tgc tgg atc gcc tgc ctc ctc ttt gaa ggc gtc gac ggc tgc   211
Lys Pro Cys Trp Ile Ala Cys Leu Leu Phe Glu Gly Val Asp Gly Cys
            25                  30                  35

gaa ggc cac tcc gac ggt gat gtt gta gct cat gca att gtg gat gct   259
Glu Gly His Ser Asp Gly Asp Val Val Ala His Ala Ile Val Asp Ala
        40                  45                  50

ctc ctt tct gcc tct ggt ctg ggg gat ttg ggc tct ttc gtt ggt gtg   307
Leu Leu Ser Ala Ser Gly Leu Gly Asp Leu Gly Ser Phe Val Gly Val
    55                  60                  65

ggg aga cct gaa tac gat ggt gtt tct ggt aca cag ttg ttg aag gaa   355
Gly Arg Pro Glu Tyr Asp Gly Val Ser Gly Thr Gln Leu Leu Lys Glu
70                  75                  80                  85

gtt cgg gag ctg ctt tcg gca cac ggg tac gtc att gga aat gtc gcc   403
Val Arg Glu Leu Leu Ser Ala His Gly Tyr Val Ile Gly Asn Val Ala
                90                  95                 100

gcc caa ctg gtt ggc caa acc ccc aaa ttt gga ccc cgc cgc gaa gaa   451
Ala Gln Leu Val Gly Gln Thr Pro Lys Phe Gly Pro Arg Arg Glu Glu
            105                 110                 115

gca caa caa gtc atc tcc gaa atc atc ggc gca cca tgc tca ctg tct   499
Ala Gln Gln Val Ile Ser Glu Ile Ile Gly Ala Pro Cys Ser Leu Ser
        120                 125                 130

gcc acc acc act gat cac atg gga ttc act ggt cgc agc gag ggt cgt   547
```

```
Ala Thr Thr Thr Asp His Met Gly Phe Thr Gly Arg Ser Glu Gly Arg
    135                 140                 145

gca tcg gta gca acg gca gtg gtg tgg aag gct taagttttct gtagggattg 600
Ala Ser Val Ala Thr Ala Val Val Trp Lys Ala
150                 155                 160

ggc                                                               603
```

<210> 2844
<211> 160
<212> PRT
<213> Corynebacterium glutamicum

<400> 2844

```
Val Thr Asn Pro Ile Ile Pro Arg Val Gly Ile Ala Thr Asp Ala His
  1               5                  10                  15

Gln Ile Glu Ala Gly Lys Pro Cys Trp Ile Ala Cys Leu Leu Phe Glu
             20                  25                  30

Gly Val Asp Gly Cys Glu Gly His Ser Asp Gly Asp Val Val Ala His
         35                  40                  45

Ala Ile Val Asp Ala Leu Leu Ser Ala Ser Gly Leu Gly Asp Leu Gly
     50                  55                  60

Ser Phe Val Gly Val Gly Arg Pro Glu Tyr Asp Gly Val Ser Gly Thr
 65                  70                  75                  80

Gln Leu Leu Lys Glu Val Arg Glu Leu Leu Ser Ala His Gly Tyr Val
                 85                  90                  95

Ile Gly Asn Val Ala Ala Gln Leu Val Gly Gln Thr Pro Lys Phe Gly
            100                 105                 110

Pro Arg Arg Glu Glu Ala Gln Gln Val Ile Ser Glu Ile Ile Gly Ala
        115                 120                 125

Pro Cys Ser Leu Ser Ala Thr Thr Thr Asp His Met Gly Phe Thr Gly
    130                 135                 140

Arg Ser Glu Gly Arg Ala Ser Val Ala Thr Ala Val Val Trp Lys Ala
145                 150                 155                 160
```

<210> 2845
<211> 705
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(682)
<223> RXA02670

<400> 2845

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ccgtttaatc aaccgactgt gtgaatgcgc ttaaacggac tagggttgtg agcagcatat 60

ccagattttt ctggataaat cctggaattt cttaaaacca atg gag gac gaa tcc   115
                                            Met Glu Asp Glu Ser
                                              1               5

gtg aag tcc ctg aac ttg gct gcc cgt cgt ggc gcg ctc gtg acc gtg   163
Val Lys Ser Leu Asn Leu Ala Ala Arg Arg Gly Ala Leu Val Thr Val
                 10                  15                  20

gct gct gcg tca gct ctt gcg ctt gca tcc tgc agt gcc gga cag atc   211
Ala Ala Ala Ser Ala Leu Ala Leu Ala Ser Cys Ser Ala Gly Gln Ile
             25                  30                  35

acc cag acc tca agc cag gtt gca gca gtt gat ggc aac cag gca ggc   259
Thr Gln Thr Ser Ser Gln Val Ala Ala Val Asp Gly Asn Gln Ala Gly
         40                  45                  50

tcc gcg aac gac cca gtt ctg gtg cgt gat gta acc gtg cac ctc acc   307
Ser Ala Asn Asp Pro Val Leu Val Arg Asp Val Thr Val His Leu Thr
     55                  60                  65

acc gac ggc gaa gct gga gta aag ttc acc gcc atc aac cag gac acc   355
Thr Asp Gly Glu Ala Gly Val Lys Phe Thr Ala Ile Asn Gln Asp Thr
 70                  75                  80                  85

tct cac act tct cac acc ctt gag tcc gtc acc gtt gac ggc gaa gag   403
Ser His Thr Ser His Thr Leu Glu Ser Val Thr Val Asp Gly Glu Glu
                 90                  95                 100

gtt gag ctt gat gat gca gag cca atc gag cgc aac tgc tcc ctc gtt   451
Val Glu Leu Asp Asp Ala Glu Pro Ile Glu Arg Asn Cys Ser Leu Val
             105                 110                 115

gca gac atc cag tcc gaa ctg gat ctg atc gag gag cca gaa gtt ggc   499
Ala Asp Ile Gln Ser Glu Leu Asp Leu Ile Glu Glu Pro Glu Val Gly
         120                 125                 130

tgc atc cag cac gta gca act tct ctg gag aac cca ggt ttc gca tac   547
Cys Ile Gln His Val Ala Thr Ser Leu Glu Asn Pro Gly Phe Ala Tyr
     135                 140                 145

ggc gga gtc gtg cca gtt gag ttc gtc ttc gac acc ggt gcg atc acc   595
Gly Gly Val Val Pro Val Glu Phe Val Phe Asp Thr Gly Ala Ile Thr
150                 155                 160                 165

atc gat gcc acc gtt tcc gca cct gtc ctc gag tca ggc gta gaa aac   643
Ile Asp Ala Thr Val Ser Ala Pro Val Leu Glu Ser Gly Val Glu Asn
                170                 175                 180

cgc gag gtc ggc gga gac act gca gag gca agc cac cac taagcctctc    692
Arg Glu Val Gly Gly Asp Thr Ala Glu Ala Ser His His
            185                 190

aaagctgctt gaa                                                   705


<210> 2846
<211> 194
<212> PRT
<213> Corynebacterium glutamicum
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<400> 2846
Met Glu Asp Glu Ser Val Lys Ser Leu Asn Leu Ala Ala Arg Arg Gly
1 5 10 15

Ala Leu Val Thr Val Ala Ala Ala Ser Ala Leu Ala Leu Ala Ser Cys
20 25 30

Ser Ala Gly Gln Ile Thr Gln Thr Ser Ser Gln Val Ala Ala Val Asp
35 40 45

Gly Asn Gln Ala Gly Ser Ala Asn Asp Pro Val Leu Val Arg Asp Val
50 55 60

Thr Val His Leu Thr Thr Asp Gly Glu Ala Gly Val Lys Phe Thr Ala
65 70 75 80

Ile Asn Gln Asp Thr Ser His Thr Ser His Thr Leu Glu Ser Val Thr
85 90 95

Val Asp Gly Glu Glu Val Glu Leu Asp Asp Ala Glu Pro Ile Glu Arg
100 105 110

Asn Cys Ser Leu Val Ala Asp Ile Gln Ser Glu Leu Asp Leu Ile Glu
115 120 125

Glu Pro Glu Val Gly Cys Ile Gln His Val Ala Thr Ser Leu Glu Asn
130 135 140

Pro Gly Phe Ala Tyr Gly Gly Val Val Pro Val Glu Phe Val Phe Asp
145 150 155 160

Thr Gly Ala Ile Thr Ile Asp Ala Thr Val Ser Ala Pro Val Leu Glu
165 170 175

Ser Gly Val Glu Asn Arg Glu Val Gly Gly Asp Thr Ala Glu Ala Ser
180 185 190

His His

<210> 2847
<211> 1221
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1198)
<223> RXA02672

<400> 2847
agcagtcatc cccggaggct caggcatcaa acaaacaagc ctgagagtca tcgaagcttc 60

aacacttgcc gaagcacttg cagcagtaag cttataaagc atg aca cca aca acc 115
Met Thr Pro Thr Thr
1 5

act cct gta tca aac cca gat gcc ctt tcc act gga act cag gat gtg 163
Thr Pro Val Ser Asn Pro Asp Ala Leu Ser Thr Gly Thr Gln Asp Val

```
                  10                  15                  20

cac acc ctc aaa gga acg ttg cag cgc ctc gcc cca ggc aca cca ctt   211
His Thr Leu Lys Gly Thr Leu Gln Arg Leu Ala Pro Gly Thr Pro Leu
             25                  30                  35

cgc gat ggc tta gac cgc atc gtc cga gga cac acc ggc gcg tta atc   259
Arg Asp Gly Leu Asp Arg Ile Val Arg Gly His Thr Gly Ala Leu Ile
         40                  45                  50

gtc att ggt gat gat gaa aac gtc tcc tcg atc tgc gac ggc ggc ttt   307
Val Ile Gly Asp Asp Glu Asn Val Ser Ser Ile Cys Asp Gly Gly Phe
     55                  60                  65

gaa ttc gac gtt tcg ttt gct gca acc cga ctc cgc gag ctg tgc aag   355
Glu Phe Asp Val Ser Phe Ala Ala Thr Arg Leu Arg Glu Leu Cys Lys
 70                  75                  80                  85

atg gat ggc gct gtc atc ttg tct tcc gac ctt gag cgt atc aaa cgc   403
Met Asp Gly Ala Val Ile Leu Ser Ser Asp Leu Glu Arg Ile Lys Arg
                 90                  95                 100

gcc aat gtt cag ctg ctg cct tca cca acc tgg cca acc cag gag tcc   451
Ala Asn Val Gln Leu Leu Pro Ser Pro Thr Trp Pro Thr Gln Glu Ser
            105                 110                 115

ggc acc cgc cac cgt tct gca gaa cgc acc gcg ctt cac acc ggt gtg   499
Gly Thr Arg His Arg Ser Ala Glu Arg Thr Ala Leu His Thr Gly Val
        120                 125                 130

cca gtg att gcg gta tcc gaa tca caa aac acc atc act ctc tac gtc   547
Pro Val Ile Ala Val Ser Glu Ser Gln Asn Thr Ile Thr Leu Tyr Val
    135                 140                 145

gag ggc aaa tcc cac atg ttg gag cag cca gct gcc ctg ctt aac cgc   595
Glu Gly Lys Ser His Met Leu Glu Gln Pro Ala Ala Leu Leu Asn Arg
150                 155                 160                 165

gcc aac caa gct ttg gga aca atg gag cgc tac cgc gat cgt ctc gat   643
Ala Asn Gln Ala Leu Gly Thr Met Glu Arg Tyr Arg Asp Arg Leu Asp
                170                 175                 180

cag gtc aat aac cgc ctt cac ctg gct gaa ctc cac agc tat gtc acc   691
Gln Val Asn Asn Arg Leu His Leu Ala Glu Leu His Ser Tyr Val Thr
            185                 190                 195

gtg att gat gtt gtt tct gtc att cag cgc gag gaa atg ctg cgc cga   739
Val Ile Asp Val Val Ser Val Ile Gln Arg Glu Glu Met Leu Arg Arg
        200                 205                 210

gtg ggt gaa atc att gat ggc gat gtt ctt gaa cta ggc aaa gac gcc   787
Val Gly Glu Ile Ile Asp Gly Asp Val Leu Glu Leu Gly Lys Asp Ala
    215                 220                 225

aag gag att cag atc cag ctc agc gaa tta cgt ggc gat aat gac cga   835
Lys Glu Ile Gln Ile Gln Leu Ser Glu Leu Arg Gly Asp Asn Asp Arg
230                 235                 240                 245

gaa cgt gaa tca atc att gct gat tac ctt gtc acc gac ggt att cct   883
Glu Arg Glu Ser Ile Ile Ala Asp Tyr Leu Val Thr Asp Gly Ile Pro
                250                 255                 260
```

```
gca gat gag gaa atc cac gca gcc ctc gaa gcg atc tca cat tta gat   931
Ala Asp Glu Glu Ile His Ala Ala Leu Glu Ala Ile Ser His Leu Asp
            265                 270                 275

gat aag gct ctg ctg aat cct gcg aac atc gcg cgt gtt ctt gga ctg   979
Asp Lys Ala Leu Leu Asn Pro Ala Asn Ile Ala Arg Val Leu Gly Leu
        280                 285                 290

cca ccg acc gag gaa gca ctt gat gag cca gtc act cct cgc ggc tac   1027
Pro Pro Thr Glu Glu Ala Leu Asp Glu Pro Val Thr Pro Arg Gly Tyr
    295                 300                 305

cgc acg ctc aac aga att cct cga gtg caa aaa ttc ctc atg gat aaa   1075
Arg Thr Leu Asn Arg Ile Pro Arg Val Gln Lys Phe Leu Met Asp Lys
310                 315                 320                 325

ctc atc gtg gaa ttc ggc aac ttg gat gca ctg ctc aat gcg tca gta   1123
Leu Ile Val Glu Phe Gly Asn Leu Asp Ala Leu Leu Asn Ala Ser Val
                330                 335                 340

gag gat cta agt gca gtc gat ggt gtg ggc tca ctg tgg gca cgc cac   1171
Glu Asp Leu Ser Ala Val Asp Gly Val Gly Ser Leu Trp Ala Arg His
            345                 350                 355

atc acc gac gga ctt ggc cgt tta agt taggttaaag gtcaccgctg         1218
Ile Thr Asp Gly Leu Gly Arg Leu Ser
        360                 365

gtg                                                               1221
```

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<210> 2848
<211> 366
<212> PRT
<213> Corynebacterium glutamicum

<400> 2848

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Met Thr Pro Thr Thr Thr Pro Val Ser Asn Pro Asp Ala Leu Ser Thr
  1               5                  10                  15

Gly Thr Gln Asp Val His Thr Leu Lys Gly Thr Leu Gln Arg Leu Ala
             20                  25                  30

Pro Gly Thr Pro Leu Arg Asp Gly Leu Asp Arg Ile Val Arg Gly His
         35                  40                  45

Thr Gly Ala Leu Ile Val Ile Gly Asp Asp Glu Asn Val Ser Ser Ile
     50                  55                  60

Cys Asp Gly Gly Phe Glu Phe Asp Val Ser Phe Ala Ala Thr Arg Leu
 65                  70                  75                  80

Arg Glu Leu Cys Lys Met Asp Gly Ala Val Ile Leu Ser Ser Asp Leu
                 85                  90                  95

Glu Arg Ile Lys Arg Ala Asn Val Gln Leu Leu Pro Ser Pro Thr Trp
            100                 105                 110

Pro Thr Gln Glu Ser Gly Thr Arg His Arg Ser Ala Glu Arg Thr Ala
        115                 120                 125
```

```
Leu His Thr Gly Val Pro Val Ile Ala Val Ser Glu Ser Gln Asn Thr
    130                 135                 140

Ile Thr Leu Tyr Val Glu Gly Lys Ser His Met Leu Glu Gln Pro Ala
145                 150                 155                 160

Ala Leu Leu Asn Arg Ala Asn Gln Ala Leu Gly Thr Met Glu Arg Tyr
                165                 170                 175

Arg Asp Arg Leu Asp Gln Val Asn Asn Arg Leu His Leu Ala Glu Leu
            180                 185                 190

His Ser Tyr Val Thr Val Ile Asp Val Val Ser Val Ile Gln Arg Glu
        195                 200                 205

Glu Met Leu Arg Arg Val Gly Glu Ile Ile Asp Gly Asp Val Leu Glu
    210                 215                 220

Leu Gly Lys Asp Ala Lys Glu Ile Gln Ile Gln Leu Ser Glu Leu Arg
225                 230                 235                 240

Gly Asp Asn Asp Arg Glu Arg Glu Ser Ile Ile Ala Asp Tyr Leu Val
                245                 250                 255

Thr Asp Gly Ile Pro Ala Asp Glu Glu Ile His Ala Ala Leu Glu Ala
            260                 265                 270

Ile Ser His Leu Asp Asp Lys Ala Leu Leu Asn Pro Ala Asn Ile Ala
        275                 280                 285

Arg Val Leu Gly Leu Pro Pro Thr Glu Glu Ala Leu Asp Glu Pro Val
    290                 295                 300

Thr Pro Arg Gly Tyr Arg Thr Leu Asn Arg Ile Pro Arg Val Gln Lys
305                 310                 315                 320

Phe Leu Met Asp Lys Leu Ile Val Glu Phe Gly Asn Leu Asp Ala Leu
                325                 330                 335

Leu Asn Ala Ser Val Glu Asp Leu Ser Ala Val Asp Gly Val Gly Ser
            340                 345                 350

Leu Trp Ala Arg His Ile Thr Asp Gly Leu Gly Arg Leu Ser
        355                 360                 365


<210> 2849
<211> 1041
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1018)
<223> RXA02678

<400> 2849
ctgtgggcgc gcgaacaggg cgtcgacatg ctcgccacca ttatccgga ccgtgcggcg 60

gagcttttga acgcacatcc caagcccgcc atgtacgcta atg cgc atg gca aag   115
```

```
                                                    Met Arg Met Ala Lys
                                                      1               5

aag act aag aag aat gaa cag ctg ccg gag ggc atg agc cgt cgt cag   163
Lys Thr Lys Lys Asn Glu Gln Leu Pro Glu Gly Met Ser Arg Arg Gln
                 10                  15                  20

gca aaa ctt gca gcc cgc gcg gct gaa cgt gca gca ctt gag cgt gaa   211
Ala Lys Leu Ala Ala Arg Ala Ala Glu Arg Ala Ala Leu Glu Arg Glu
             25                  30                  35

cct cgc cca ttc gag ggc ctg gca atg gag tca cag ctc gtt gca ctg   259
Pro Arg Pro Phe Glu Gly Leu Ala Met Glu Ser Gln Leu Val Ala Leu
         40                  45                  50

cag gaa ttc att cca tct gca acc gca ccc atc acc gtt gca ggc acc   307
Gln Glu Phe Ile Pro Ser Ala Thr Ala Pro Ile Thr Val Ala Gly Thr
     55                  60                  65

gat cgc aag atc acc ctc tgt acc gtg ctt cca ggc gca gct gcg gca   355
Asp Arg Lys Ile Thr Leu Cys Thr Val Leu Pro Gly Ala Ala Ala Ala
 70                  75                  80                  85

ctt gtc cgc gaa gaa gca ttc ggc ggc gaa gcg ttt gtt gca atg cag   403
Leu Val Arg Glu Glu Ala Phe Gly Gly Glu Ala Phe Val Ala Met Gln
                 90                  95                 100

cag gcc atc cgc tcc aac aac cca agc aag gac ctc gcg ttc gcg ctg   451
Gln Ala Ile Arg Ser Asn Asn Pro Ser Lys Asp Leu Ala Phe Ala Leu
            105                 110                 115

aac tgg gtc atc aac gca aaa gcc ggc gag tca ctg gcc acc gcc aca   499
Asn Trp Val Ile Asn Ala Lys Ala Gly Glu Ser Leu Ala Thr Ala Thr
        120                 125                 130

gcg gac ggc acc cag cca gag cta aag agc ttg ctt aac gac gcc gac   547
Ala Asp Gly Thr Gln Pro Glu Leu Lys Ser Leu Leu Asn Asp Ala Asp
    135                 140                 145

acc ctc gaa atc acc act cac cag gac ttc aac tgg tgg ctg gcg gaa   595
Thr Leu Glu Ile Thr Thr His Gln Asp Phe Asn Trp Trp Leu Ala Glu
150                 155                 160                 165

aac gac aac ctc tcc cca gaa gtt gcg cag cac atg cag gca gcc aat   643
Asn Asp Asn Leu Ser Pro Glu Val Ala Gln His Met Gln Ala Ala Asn
                170                 175                 180

gac tcc atc ctg cct tca cac gaa gtc gaa gca gac gtc cca ggc gct   691
Asp Ser Ile Leu Pro Ser His Glu Val Glu Ala Asp Val Pro Gly Ala
            185                 190                 195

gtt tgg tgg gtc aac cca ggc gga aaa gcg cac atc cgt tgg gtc cgc   739
Val Trp Trp Val Asn Pro Gly Gly Lys Ala His Ile Arg Trp Val Arg
        200                 205                 210

acc gaa aac gaa acc gca ctg ttc aac gct ttg gca cgc atc gca gca   787
Thr Glu Asn Glu Thr Ala Leu Phe Asn Ala Leu Ala Arg Ile Ala Ala
    215                 220                 225

cgt ggc gag ctg aat ctc ggc gaa gaa act aag ttc gct ggt gct ttc   835
Arg Gly Glu Leu Asn Leu Gly Glu Glu Thr Lys Phe Ala Gly Ala Phe
```

```
230                 235                 240                 245

cgc acc cac ggc atc gtc gtc cca gtg tgg gat ctc gat cct gag cgt   883
Arg Thr His Gly Ile Val Val Pro Val Trp Asp Leu Asp Pro Glu Arg
                250                 255                 260

cca tcc acc gat tac gcc gat gtt ttg gtt gca ctc aac gag aag atc   931
Pro Ser Thr Asp Tyr Ala Asp Val Leu Val Ala Leu Asn Glu Lys Ile
            265                 270                 275

gtc gct gaa ctg gat aac gat gca cag ctc aac gcc gac gag cgc cgt   979
Val Ala Glu Leu Asp Asn Asp Ala Gln Leu Asn Ala Asp Glu Arg Arg
        280                 285                 290

cag ctg gag aac atc aag tcc cgc cag gtg acc atc cgc taaaatctct   1028
Gln Leu Glu Asn Ile Lys Ser Arg Gln Val Thr Ile Arg
    295                 300                 305

taaaaacact tca                                                  1041
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<210> 2850
<211> 306
<212> PRT
<213> Corynebacterium glutamicum

<400> 2850

```
Met Arg Met Ala Lys Lys Thr Lys Lys Asn Glu Gln Leu Pro Glu Gly
  1               5                  10                  15

Met Ser Arg Arg Gln Ala Lys Leu Ala Ala Arg Ala Ala Glu Arg Ala
             20                  25                  30

Ala Leu Glu Arg Glu Pro Arg Pro Phe Glu Gly Leu Ala Met Glu Ser
         35                  40                  45

Gln Leu Val Ala Leu Gln Glu Phe Ile Pro Ser Ala Thr Ala Pro Ile
     50                  55                  60

Thr Val Ala Gly Thr Asp Arg Lys Ile Thr Leu Cys Thr Val Leu Pro
 65                  70                  75                  80

Gly Ala Ala Ala Ala Leu Val Arg Glu Glu Ala Phe Gly Gly Glu Ala
                 85                  90                  95

Phe Val Ala Met Gln Gln Ala Ile Arg Ser Asn Asn Pro Ser Lys Asp
            100                 105                 110

Leu Ala Phe Ala Leu Asn Trp Val Ile Asn Ala Lys Ala Gly Glu Ser
        115                 120                 125

Leu Ala Thr Ala Thr Ala Asp Gly Thr Gln Pro Glu Leu Lys Ser Leu
    130                 135                 140

Leu Asn Asp Ala Asp Thr Leu Glu Ile Thr Thr His Gln Asp Phe Asn
145                 150                 155                 160

Trp Trp Leu Ala Glu Asn Asp Asn Leu Ser Pro Glu Val Ala Gln His
                165                 170                 175

Met Gln Ala Ala Asn Asp Ser Ile Leu Pro Ser His Glu Val Glu Ala
```

```
            180                 185                 190

Asp Val Pro Gly Ala Val Trp Trp Val Asn Pro Gly Gly Lys Ala His
        195                 200                 205

Ile Arg Trp Val Arg Thr Glu Asn Glu Thr Ala Leu Phe Asn Ala Leu
    210                 215                 220

Ala Arg Ile Ala Ala Arg Gly Glu Leu Asn Leu Gly Glu Glu Thr Lys
225                 230                 235                 240

Phe Ala Gly Ala Phe Arg Thr His Gly Ile Val Val Pro Val Trp Asp
                245                 250                 255

Leu Asp Pro Glu Arg Pro Ser Thr Asp Tyr Ala Asp Val Leu Val Ala
            260                 265                 270

Leu Asn Glu Lys Ile Val Ala Glu Leu Asp Asn Asp Ala Gln Leu Asn
        275                 280                 285

Ala Asp Glu Arg Arg Gln Leu Glu Asn Ile Lys Ser Arg Gln Val Thr
    290                 295                 300

Ile Arg
305


<210> 2851
<211> 801
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(778)
<223> RXA02683

<400> 2851
gacggtttct tctgtcatga cggaaactcc tacttatacc tcttcatcta ggtcggtgga 60

atctaccgcg gggacgatcg ctgcctcgga ggaagccacg atg acg cta ctg gag   115
                                              Met Thr Leu Leu Glu
                                                1               5

aat agt tcg ggg gat ccg gga tct gat tct ggg ggt gca cgc tat agc   163
Asn Ser Ser Gly Asp Pro Gly Ser Asp Ser Gly Gly Ala Arg Tyr Ser
                10                  15                  20

ctc aat tcg ctc aaa gtt tct gag cag gcc gcg gct aac gcc gtc tta   211
Leu Asn Ser Leu Lys Val Ser Glu Gln Ala Ala Ala Asn Ala Val Leu
            25                  30                  35

aag gcc gtg ctt aac gac gtc tcc tac caa gag ttc gca gac tcc tcc   259
Lys Ala Val Leu Asn Asp Val Ser Tyr Gln Glu Phe Ala Asp Ser Ser
        40                  45                  50

tac tta gaa atc aca gga acg ccc tcc gcc gac gga aca tgg ggc atc   307
Tyr Leu Glu Ile Thr Gly Thr Pro Ser Ala Asp Gly Thr Trp Gly Ile
    55                  60                  65

tca ttt ggc gga cct tcc gaa tcg gcc tcc gtg gaa ttc tcc gac ggc   355
```

```
Ser Phe Gly Gly Pro Ser Glu Ser Ala Ser Val Glu Phe Ser Asp Gly
 70                  75                  80                  85

agc atc agc ttc tcc cct gtt gac atg aca gtg ccc gca aca cga ttg   403
Ser Ile Ser Phe Ser Pro Val Asp Met Thr Val Pro Ala Thr Arg Leu
                90                  95                 100

cct cag atg ggc gca ttt tat gaa acc ctg acc gaa gaa caa tta ggc   451
Pro Gln Met Gly Ala Phe Tyr Glu Thr Leu Thr Glu Glu Gln Leu Gly
            105                 110                 115

atg ctg gag act ggc ctc gcg gtt tcc acc gtg gat tcg agc caa cag   499
Met Leu Glu Thr Gly Leu Ala Val Ser Thr Val Asp Ser Ser Gln Gln
        120                 125                 130

gaa atg ctt ctg gac ttg gtc tcc aac tcg atc ggc ctg gca gat act   547
Glu Met Leu Leu Asp Leu Val Ser Asn Ser Ile Gly Leu Ala Asp Thr
    135                 140                 145

gaa acc act gcg act gca att agt aaa atc cga gca acg ctt tcc gag   595
Glu Thr Thr Ala Thr Ala Ile Ser Lys Ile Arg Ala Thr Leu Ser Glu
150                 155                 160                 165

acc tac ctg ttc gga acc ccc gac gga tta acc ttg gcg ctt agt ggc   643
Thr Tyr Leu Phe Gly Thr Pro Asp Gly Leu Thr Leu Ala Leu Ser Gly
                170                 175                 180

cca cac gtt gat ttc gaa gtc tcc cac cag ggc agc acc gcg aaa att   691
Pro His Val Asp Phe Glu Val Ser His Gln Gly Ser Thr Ala Lys Ile
            185                 190                 195

act tac cgc gat cca agc acc gac acc tta acc gcc gaa gat cgg gta   739
Thr Tyr Arg Asp Pro Ser Thr Asp Thr Leu Thr Ala Glu Asp Arg Val
        200                 205                 210

gat acc gca agt gtg gct gct gct ccg ccg gag gtt gtt taggcgtttg    788
Asp Thr Ala Ser Val Ala Ala Ala Pro Pro Glu Val Val
    215                 220                 225

ccgagaaatt ttc                                                   801


<210> 2852
<211> 226
<212> PRT
<213> Corynebacterium glutamicum

<400> 2852
Met Thr Leu Leu Glu Asn Ser Ser Gly Asp Pro Gly Ser Asp Ser Gly
  1               5                  10                  15

Gly Ala Arg Tyr Ser Leu Asn Ser Leu Lys Val Ser Glu Gln Ala Ala
             20                  25                  30

Ala Asn Ala Val Leu Lys Ala Val Leu Asn Asp Val Ser Tyr Gln Glu
         35                  40                  45

Phe Ala Asp Ser Ser Tyr Leu Glu Ile Thr Gly Thr Pro Ser Ala Asp
     50                  55                  60

Gly Thr Trp Gly Ile Ser Phe Gly Gly Pro Ser Glu Ser Ala Ser Val
```

```
 65                  70                  75                  80

Glu Phe Ser Asp Gly Ser Ile Ser Phe Ser Pro Val Asp Met Thr Val
                 85                  90                  95

Pro Ala Thr Arg Leu Pro Gln Met Gly Ala Phe Tyr Glu Thr Leu Thr
            100                 105                 110

Glu Glu Gln Leu Gly Met Leu Glu Thr Gly Leu Ala Val Ser Thr Val
        115                 120                 125

Asp Ser Ser Gln Gln Glu Met Leu Leu Asp Leu Val Ser Asn Ser Ile
    130                 135                 140

Gly Leu Ala Asp Thr Glu Thr Thr Ala Thr Ala Ile Ser Lys Ile Arg
145                 150                 155                 160

Ala Thr Leu Ser Glu Thr Tyr Leu Phe Gly Thr Pro Asp Gly Leu Thr
                165                 170                 175

Leu Ala Leu Ser Gly Pro His Val Asp Phe Glu Val Ser His Gln Gly
            180                 185                 190

Ser Thr Ala Lys Ile Thr Tyr Arg Asp Pro Ser Thr Asp Thr Leu Thr
        195                 200                 205

Ala Glu Asp Arg Val Asp Thr Ala Ser Val Ala Ala Ala Pro Pro Glu
    210                 215                 220

Val Val
225


<210> 2853
<211> 780
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(757)
<223> RXA02685

<400> 2853
tagcagcatt tgtggaaaga gctgtggcat gagtagttca gtaatgtcac cgcgtcgaat 60

aaaggcggaa atacttatcg ttttagccat caccttggc atg agc ggc ctg cga   115
                                            Met Ser Gly Leu Arg
                                              1               5

tca atc ctg cgc ctc atc gac gat ctc ctc gca ccg gtt gcg ctc aac   163
Ser Ile Leu Arg Leu Ile Asp Asp Leu Leu Ala Pro Val Ala Leu Asn
                10                  15                  20

gac cag caa gtt gca ctg aat gcc tca atg gca aac tcc gca tgg ctg   211
Asp Gln Gln Val Ala Leu Asn Ala Ser Met Ala Asn Ser Ala Trp Leu
            25                  30                  35

gat ctc acc ttg caa ttg tgt tcc gcc gga gtg ctg ttt tcc tgg gga   259
Asp Leu Thr Leu Gln Leu Cys Ser Ala Gly Val Leu Phe Ser Trp Gly
        40                  45                  50
```

```
gca cta gcg atc tac ctg cta ggt gaa cgt ttt cag tgg att aaa ccc   307
Ala Leu Ala Ile Tyr Leu Leu Gly Glu Arg Phe Gln Trp Ile Lys Pro
     55                  60                  65

aaa gac tgg gca tgg ggt gca ggc ctt gca gca ctc att ggt att cca   355
Lys Asp Trp Ala Trp Gly Ala Gly Leu Ala Ala Leu Ile Gly Ile Pro
 70                  75                  80                  85

ggg tta atc ttc tac gcc agt gct gtt cat ttg ggg ctg tcc aaa cag   403
Gly Leu Ile Phe Tyr Ala Ser Ala Val His Leu Gly Leu Ser Lys Gln
                 90                  95                 100

gtt gtg ccc acc acg ttg gaa acc tgg tgg gaa atc cca gta ctt ctt   451
Val Val Pro Thr Thr Leu Glu Thr Trp Trp Glu Ile Pro Val Leu Leu
            105                 110                 115

atc tgg tca gct gcc aac gcc ttt ggt gaa gag atc gtg gta gtc atg   499
Ile Trp Ser Ala Ala Asn Ala Phe Gly Glu Glu Ile Val Val Val Met
        120                 125                 130

tgg ttt ttc acc agg ctg cgc cag ctg aag tgg agt gtg cct gca gtt   547
Trp Phe Phe Thr Arg Leu Arg Gln Leu Lys Trp Ser Val Pro Ala Val
    135                 140                 145

atc gtg aca tct tca gta cta cgc ggt tcc tat cac ctc tac cag gga   595
Ile Val Thr Ser Ser Val Leu Arg Gly Ser Tyr His Leu Tyr Gln Gly
150                 155                 160                 165

atc tct gca ggc ttg ggc aac atc atc atg gga gta gcg ttc gcg tac   643
Ile Ser Ala Gly Leu Gly Asn Ile Ile Met Gly Val Ala Phe Ala Tyr
                170                 175                 180

ttc tat cac cgc acg ggc aaa atc tgg cca ctg gta atc gct cac ttc   691
Phe Tyr His Arg Thr Gly Lys Ile Trp Pro Leu Val Ile Ala His Phe
            185                 190                 195

ttg att gat gcg gtg gct ttt gtg ggc tac tcc gca att ggc ggg aat   739
Leu Ile Asp Ala Val Ala Phe Val Gly Tyr Ser Ala Ile Gly Gly Asn
        200                 205                 210

tta agt tgg tta ggg ctt taaactgaag ttcctatttt att                 780
Leu Ser Trp Leu Gly Leu
    215
```

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<210> 2854
<211> 219
<212> PRT
<213> Corynebacterium glutamicum

<400> 2854

```
Met Ser Gly Leu Arg Ser Ile Leu Arg Leu Ile Asp Asp Leu Leu Ala
  1               5                  10                  15

Pro Val Ala Leu Asn Asp Gln Gln Val Ala Leu Asn Ala Ser Met Ala
             20                  25                  30

Asn Ser Ala Trp Leu Asp Leu Thr Leu Gln Leu Cys Ser Ala Gly Val
         35                  40                  45
```

```
Leu Phe Ser Trp Gly Ala Leu Ala Ile Tyr Leu Leu Gly Glu Arg Phe
     50                  55                  60

Gln Trp Ile Lys Pro Lys Asp Trp Ala Trp Gly Ala Gly Leu Ala Ala
 65                  70                  75                  80

Leu Ile Gly Ile Pro Gly Leu Ile Phe Tyr Ala Ser Ala Val His Leu
                85                  90                  95

Gly Leu Ser Lys Gln Val Val Pro Thr Thr Leu Glu Thr Trp Trp Glu
            100                 105                 110

Ile Pro Val Leu Leu Ile Trp Ser Ala Ala Asn Ala Phe Gly Glu Glu
        115                 120                 125

Ile Val Val Val Met Trp Phe Phe Thr Arg Leu Arg Gln Leu Lys Trp
    130                 135                 140

Ser Val Pro Ala Val Ile Val Thr Ser Ser Val Leu Arg Gly Ser Tyr
145                 150                 155                 160

His Leu Tyr Gln Gly Ile Ser Ala Gly Leu Gly Asn Ile Ile Met Gly
                165                 170                 175

Val Ala Phe Ala Tyr Phe Tyr His Arg Thr Gly Lys Ile Trp Pro Leu
            180                 185                 190

Val Ile Ala His Phe Leu Ile Asp Ala Val Ala Phe Val Gly Tyr Ser
        195                 200                 205

Ala Ile Gly Gly Asn Leu Ser Trp Leu Gly Leu
    210                 215


<210> 2855
<211> 792
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(769)
<223> RXA02688

<400> 2855
gtgcggaaga cagcacgccc caaaccgacc aactagctaa gctacacaag gcggacgaat 60

gggttcgcgc agcaagcgaa ggaaggaaac ttaactagcc atg gcc ggc cgg att   115
                                              Met Ala Gly Arg Ile
                                                1               5

att ttg cta cga cac ggg cag act cac aac aac gtc aaa cac ctc ctg   163
Ile Leu Leu Arg His Gly Gln Thr His Asn Asn Val Lys His Leu Leu
                10                  15                  20

gac acc cgc cca cca gga gct gaa ctc acc gac ctg ggc cgt aaa caa   211
Asp Thr Arg Pro Pro Gly Ala Glu Leu Thr Asp Leu Gly Arg Lys Gln
            25                  30                  35

gcc ctt gaa gtt ggc cac gaa cta gcc acc tac tcc ggt gag cgc ctc   259
Ala Leu Glu Val Gly His Glu Leu Ala Thr Tyr Ser Gly Glu Arg Leu
```

```
         40                  45                  50

gcc cat gtg tac agc tcc atc gtg ttg cgc gcc caa caa acc gcc gtg   307
Ala His Val Tyr Ser Ser Ile Val Leu Arg Ala Gln Gln Thr Ala Val
     55                  60                  65

ctt gcc acc tct acc ttt gaa aaa gct cgc gac atg cag tcc ggt gcg   355
Leu Ala Thr Ser Thr Phe Glu Lys Ala Arg Asp Met Gln Ser Gly Ala
 70                  75                  80                  85

att cca ctc gac gtt gtg gaa ggc att cag gaa atc aac gtc ggc gac   403
Ile Pro Leu Asp Val Val Glu Gly Ile Gln Glu Ile Asn Val Gly Asp
                90                  95                 100

ttt gaa atg cgc ggc gat gaa gaa gcc cac atg aat tac tcc cgc gca   451
Phe Glu Met Arg Gly Asp Glu Glu Ala His Met Asn Tyr Ser Arg Ala
            105                 110                 115

ctc aac ggc tgg ctt cac ggg gat cct gcc gct ggt ctt ccc ggc ggt   499
Leu Asn Gly Trp Leu His Gly Asp Pro Ala Ala Gly Leu Pro Gly Gly
        120                 125                 130

gag acc tac aaa gac gtg ctg aac cgc tac cag ccg act ctt gat cga   547
Glu Thr Tyr Lys Asp Val Leu Asn Arg Tyr Gln Pro Thr Leu Asp Arg
    135                 140                 145

atc atg gac agc cac gac ctt gac gac gac cgc gac gtt gcc gtt gtc   595
Ile Met Asp Ser His Asp Leu Asp Asp Asp Arg Asp Val Ala Val Val
150                 155                 160                 165

agc cac ggc gcc gtc atc cgc atc gtg gca aca cac gca act ggt gtg   643
Ser His Gly Ala Val Ile Arg Ile Val Ala Thr His Ala Thr Gly Val
                170                 175                 180

gat ccc aac ttt gcg ttc aac acc tac ctg ggc aac tgc cgc ttc gtg   691
Asp Pro Asn Phe Ala Phe Asn Thr Tyr Leu Gly Asn Cys Arg Phe Val
            185                 190                 195

gtg ctg gag cca aac ggt aag aaa ttc agc caa tgg gat gtt gtg cgc   739
Val Leu Glu Pro Asn Gly Lys Lys Phe Ser Gln Trp Asp Val Val Arg
        200                 205                 210

tgg act gac agc cca ctg cca tgg cag gag taattgagac caaaggctcg     789
Trp Thr Asp Ser Pro Leu Pro Trp Gln Glu
    215                 220

gat                                                               792
```

US 20050153417A1 20050714

<210> 2856
<211> 223
<212> PRT
<213> Corynebacterium glutamicum

<400> 2856

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Met Ala Gly Arg Ile Ile Leu Leu Arg His Gly Gln Thr His Asn Asn
  1               5                  10                  15

Val Lys His Leu Leu Asp Thr Arg Pro Pro Gly Ala Glu Leu Thr Asp
             20                  25                  30
```

```
Leu Gly Arg Lys Gln Ala Leu Glu Val Gly His Glu Leu Ala Thr Tyr
         35                  40                  45

Ser Gly Glu Arg Leu Ala His Val Tyr Ser Ser Ile Val Leu Arg Ala
     50                  55                  60

Gln Gln Thr Ala Val Leu Ala Thr Ser Thr Phe Glu Lys Ala Arg Asp
 65                  70                  75                  80

Met Gln Ser Gly Ala Ile Pro Leu Asp Val Val Glu Gly Ile Gln Glu
                 85                  90                  95

Ile Asn Val Gly Asp Phe Glu Met Arg Gly Asp Glu Glu Ala His Met
            100                 105                 110

Asn Tyr Ser Arg Ala Leu Asn Gly Trp Leu His Gly Asp Pro Ala Ala
        115                 120                 125

Gly Leu Pro Gly Gly Glu Thr Tyr Lys Asp Val Leu Asn Arg Tyr Gln
    130                 135                 140

Pro Thr Leu Asp Arg Ile Met Asp Ser His Asp Leu Asp Asp Asp Arg
145                 150                 155                 160

Asp Val Ala Val Val Ser His Gly Ala Val Ile Arg Ile Val Ala Thr
                165                 170                 175

His Ala Thr Gly Val Asp Pro Asn Phe Ala Phe Asn Thr Tyr Leu Gly
            180                 185                 190

Asn Cys Arg Phe Val Val Leu Glu Pro Asn Gly Lys Lys Phe Ser Gln
        195                 200                 205

Trp Asp Val Val Arg Trp Thr Asp Ser Pro Leu Pro Trp Gln Glu
    210                 215                 220
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<210> 2857
<211> 465
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(442)
<223> RXA02689

<400> 2857

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gtgaagttcc cccacctcag ccagagcgcg atccgctccg tgacactgca ggaacgacag 60

catccgcgga ggtcggagta cctgtagagg agaacgctcc atg att gaa gtc agc   115
                                            Met Ile Glu Val Ser
                                              1               5

gac gaa cgc ttc gag gaa ctg gtc gaa cta gcc ttc gac caa gtt ccc   163
Asp Glu Arg Phe Glu Glu Leu Val Glu Leu Ala Phe Asp Gln Val Pro
                 10                  15                  20

cag caa ttc ctg gat cat atg cgc aac gtg gtt tta ctc att gag gat   211
Gln Gln Phe Leu Asp His Met Arg Asn Val Val Leu Leu Ile Glu Asp
             25                  30                  35
```

```
ttc aac cca gat tcg cct tat atc ttg ggt tta tac cac ggc gtt gct   259
Phe Asn Pro Asp Ser Pro Tyr Ile Leu Gly Leu Tyr His Gly Val Ala
         40                  45                  50

ctc aca gag cgc aca ttc aac cac ggt ggc ctg ccg gat tcc atc acc   307
Leu Thr Glu Arg Thr Phe Asn His Gly Gly Leu Pro Asp Ser Ile Thr
     55                  60                  65

att tat aaa ggt gcg ttg caa aat tac tgc aat tca gag gaa caa cta   355
Ile Tyr Lys Gly Ala Leu Gln Asn Tyr Cys Asn Ser Glu Glu Gln Leu
 70                  75                  80                  85

gtg gag cag gtg cgg gtg acc gtg ctg cat gag att ggg cat tat ttt   403
Val Glu Gln Val Arg Val Thr Val Leu His Glu Ile Gly His Tyr Phe
                 90                  95                 100

ggc ctc ggc gaa gag gac ctg cac agg ctc gga tac gcc taaaacgcct    452
Gly Leu Gly Glu Glu Asp Leu His Arg Leu Gly Tyr Ala
            105                 110

cattaggtgc aca                                                   465


<210> 2858
<211> 114
<212> PRT
<213> Corynebacterium glutamicum

<400> 2858
Met Ile Glu Val Ser Asp Glu Arg Phe Glu Glu Leu Val Glu Leu Ala
  1               5                  10                  15

Phe Asp Gln Val Pro Gln Gln Phe Leu Asp His Met Arg Asn Val Val
             20                  25                  30

Leu Leu Ile Glu Asp Phe Asn Pro Asp Ser Pro Tyr Ile Leu Gly Leu
         35                  40                  45

Tyr His Gly Val Ala Leu Thr Glu Arg Thr Phe Asn His Gly Gly Leu
     50                  55                  60

Pro Asp Ser Ile Thr Ile Tyr Lys Gly Ala Leu Gln Asn Tyr Cys Asn
 65                  70                  75                  80

Ser Glu Glu Gln Leu Val Glu Gln Val Arg Val Thr Val Leu His Glu
                 85                  90                  95

Ile Gly His Tyr Phe Gly Leu Gly Glu Glu Asp Leu His Arg Leu Gly
            100                 105                 110

Tyr Ala


<210> 2859
<211> 1221
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<221> CDS
<222> (101)..(1198)
<223> RXA02690

<400> 2859
tttccttgta ccgaaccgac cgatattctt taaaaacatt ggttacacgc tccgaagatc 60

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tctgacgtga acccattttg gtggcatgat ggtgtcaatt atg agt aca aac ttt   115
                                             Met Ser Thr Asn Phe
                                               1               5

gac act tcg acg tct cca gag ggt gaa acc aag aag aac tct tct ttc   163
Asp Thr Ser Thr Ser Pro Glu Gly Glu Thr Lys Lys Asn Ser Ser Phe
                10                  15                  20

cgc act gcg gcc tct gtg cag acc atg ctt gtt gca gct ttg gca gca   211
Arg Thr Ala Ala Ser Val Gln Thr Met Leu Val Ala Ala Leu Ala Ala
            25                  30                  35

acg gct gct gtt ggc gtg tac tcc tac aac acg gac aat tca gca aac   259
Thr Ala Ala Val Gly Val Tyr Ser Tyr Asn Thr Asp Asn Ser Ala Asn
        40                  45                  50

ggc ggc gaa tcc ccc aca gga cct gag caa agt aca gtg tcc acc acc   307
Gly Gly Glu Ser Pro Thr Gly Pro Glu Gln Ser Thr Val Ser Thr Thr
    55                  60                  65

gca act att gcc tca ttt acc act gct gac gtg ggc caa tgt gca acc   355
Ala Thr Ile Ala Ser Phe Thr Thr Ala Asp Val Gly Gln Cys Ala Thr
70                  75                  80                  85

tgg gat gtt aac aat gaa ggt cta gtg tct ggt ttt gaa caa acc agc   403
Trp Asp Val Asn Asn Glu Gly Leu Val Ser Gly Phe Glu Gln Thr Ser
                90                  95                 100

tgc gat caa gag cac cgc ttt gaa att tct gct cgg gaa aac ttg gca   451
Cys Asp Gln Glu His Arg Phe Glu Ile Ser Ala Arg Glu Asn Leu Ala
            105                 110                 115

act tac cca agt tcg gaa ttc ggt ccg gac gca gct cca cca aac ctc   499
Thr Tyr Pro Ser Ser Glu Phe Gly Pro Asp Ala Ala Pro Pro Asn Leu
        120                 125                 130

acc cgt cag gcg cag ctg cgt gaa gag ctc tgc caa tct cct acc ttg   547
Thr Arg Gln Ala Gln Leu Arg Glu Glu Leu Cys Gln Ser Pro Thr Leu
    135                 140                 145

gcg tat ttg aat aac cgt ttc gat cca tcg ggg cgc tac acc atc gcc   595
Ala Tyr Leu Asn Asn Arg Phe Asp Pro Ser Gly Arg Tyr Thr Ile Ala
150                 155                 160                 165

ccg atc ctg cca cct gcg gaa gcg tgg gct gcg gga gat cgc acc atg   643
Pro Ile Leu Pro Pro Ala Glu Ala Trp Ala Ala Gly Asp Arg Thr Met
                170                 175                 180

ctc tgt gga ctt cag gca acc gac gct tca ggc act cca caa ctc acc   691
Leu Cys Gly Leu Gln Ala Thr Asp Ala Ser Gly Thr Pro Gln Leu Thr
            185                 190                 195

gtc gga ccg ata gca gcc aat gac cag gca cgc gtt ttt gaa acc ggc   739
Val Gly Pro Ile Ala Ala Asn Asp Gln Ala Arg Val Phe Glu Thr Gly
```

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        200                 205                 210

gcc tgc gtg aag gtg gaa tcc tcc gca gag ttc cgc caa gtt gat tgc   787
Ala Cys Val Lys Val Glu Ser Ser Ala Glu Phe Arg Gln Val Asp Cys
    215                 220                 225

acg gaa gat cac cac ctc gaa tca att ttg aca gtc aac ctt ggt gtc   835
Thr Glu Asp His His Leu Glu Ser Ile Leu Thr Val Asn Leu Gly Val
230                 235                 240                 245

ccc ttc cca cag ggc gcg ccc agc acg gat gag cag aac aat ttc ctc   883
Pro Phe Pro Gln Gly Ala Pro Ser Thr Asp Glu Gln Asn Asn Phe Leu
                250                 255                 260

gga aac acc tgc acc caa gca tcc att gat tac cta ggc tcc gaa gaa   931
Gly Asn Thr Cys Thr Gln Ala Ser Ile Asp Tyr Leu Gly Ser Glu Glu
            265                 270                 275

aac gtc tac caa tcc acc ctg cag acc ttc tgg cca acg att acc tcc   979
Asn Val Tyr Gln Ser Thr Leu Gln Thr Phe Trp Pro Thr Ile Thr Ser
        280                 285                 290

aac tcc tgg ttg ggc ggt tca cac agc gtg aac tgc ttc ctc atg tca   1027
Asn Ser Trp Leu Gly Gly Ser His Ser Val Asn Cys Phe Leu Met Ser
    295                 300                 305

cca tcc acc gag ggt gct gca aca ttt aac acc ctc aac ggt tca gcg   1075
Pro Ser Thr Glu Gly Ala Ala Thr Phe Asn Thr Leu Asn Gly Ser Ala
310                 315                 320                 325

act ggc aca ttc acc atc aac ggt gaa gtt ccc cca cct cag cca gag   1123
Thr Gly Thr Phe Thr Ile Asn Gly Glu Val Pro Pro Pro Gln Pro Glu
                330                 335                 340

cgc gat ccg ctc cgt gac act gca gga acg aca gca tcc gcg gag gtc   1171
Arg Asp Pro Leu Arg Asp Thr Ala Gly Thr Thr Ala Ser Ala Glu Val
            345                 350                 355

gga gta cct gta gag gag aac gct cca tgattgaagt cagcgacgaa         1218
Gly Val Pro Val Glu Glu Asn Ala Pro
        360                 365

cgc                                                              1221


<210> 2860
<211> 366
<212> PRT
<213> Corynebacterium glutamicum

<400> 2860
Met Ser Thr Asn Phe Asp Thr Ser Thr Ser Pro Glu Gly Glu Thr Lys
  1               5                  10                  15

Lys Asn Ser Ser Phe Arg Thr Ala Ala Ser Val Gln Thr Met Leu Val
             20                  25                  30

Ala Ala Leu Ala Ala Thr Ala Ala Val Gly Val Tyr Ser Tyr Asn Thr
         35                  40                  45

Asp Asn Ser Ala Asn Gly Gly Glu Ser Pro Thr Gly Pro Glu Gln Ser
```

```
     50                  55                  60

Thr Val Ser Thr Thr Ala Thr Ile Ala Ser Phe Thr Thr Ala Asp Val
 65                  70                  75                  80

Gly Gln Cys Ala Thr Trp Asp Val Asn Asn Glu Gly Leu Val Ser Gly
                 85                  90                  95

Phe Glu Gln Thr Ser Cys Asp Gln Glu His Arg Phe Glu Ile Ser Ala
            100                 105                 110

Arg Glu Asn Leu Ala Thr Tyr Pro Ser Ser Glu Phe Gly Pro Asp Ala
        115                 120                 125

Ala Pro Pro Asn Leu Thr Arg Gln Ala Gln Leu Arg Glu Glu Leu Cys
    130                 135                 140

Gln Ser Pro Thr Leu Ala Tyr Leu Asn Asn Arg Phe Asp Pro Ser Gly
145                 150                 155                 160

Arg Tyr Thr Ile Ala Pro Ile Leu Pro Pro Ala Glu Ala Trp Ala Ala
                165                 170                 175

Gly Asp Arg Thr Met Leu Cys Gly Leu Gln Ala Thr Asp Ala Ser Gly
            180                 185                 190

Thr Pro Gln Leu Thr Val Gly Pro Ile Ala Ala Asn Asp Gln Ala Arg
        195                 200                 205

Val Phe Glu Thr Gly Ala Cys Val Lys Val Glu Ser Ser Ala Glu Phe
    210                 215                 220

Arg Gln Val Asp Cys Thr Glu Asp His His Leu Glu Ser Ile Leu Thr
225                 230                 235                 240

Val Asn Leu Gly Val Pro Phe Pro Gln Gly Ala Pro Ser Thr Asp Glu
                245                 250                 255

Gln Asn Asn Phe Leu Gly Asn Thr Cys Thr Gln Ala Ser Ile Asp Tyr
            260                 265                 270

Leu Gly Ser Glu Glu Asn Val Tyr Gln Ser Thr Leu Gln Thr Phe Trp
        275                 280                 285

Pro Thr Ile Thr Ser Asn Ser Trp Leu Gly Gly Ser His Ser Val Asn
    290                 295                 300

Cys Phe Leu Met Ser Pro Ser Thr Glu Gly Ala Ala Thr Phe Asn Thr
305                 310                 315                 320

Leu Asn Gly Ser Ala Thr Gly Thr Phe Thr Ile Asn Gly Glu Val Pro
                325                 330                 335

Pro Pro Gln Pro Glu Arg Asp Pro Leu Arg Asp Thr Ala Gly Thr Thr
            340                 345                 350

Ala Ser Ala Glu Val Gly Val Pro Val Glu Glu Asn Ala Pro
        355                 360                 365
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<210> 2861

<211> 1359
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1336)
<223> RXA02700

<400> 2861
tgacaactga tgcggacgac aacgatcgaa tttatagtca aacccctcgt gcacgcagcg 60

aagtctcggt agggggagaa gttacagtaa gggcgtttta gtg gtt ccc tcg ttg 115
Val Val Pro Ser Leu
1 5

cag caa tgg cga aaa cct gct ctc atc ctg gcc att ttg acg gtg cta 163
Gln Gln Trp Arg Lys Pro Ala Leu Ile Leu Ala Ile Leu Thr Val Leu
10 15 20

ggc gta ctc ctg acc cat tgg ttc gcc tgg cca ctc acc tgg ccg ctg 211
Gly Val Leu Leu Thr His Trp Phe Ala Trp Pro Leu Thr Trp Pro Leu
25 30 35

ggg ctg cgt ctt ccc gtt gat gta gag gtg tac tgg cag ggt gcg cgc 259
Gly Leu Arg Leu Pro Val Asp Val Glu Val Tyr Trp Gln Gly Ala Arg
40 45 50

gag ttt tgg ctc gcc gat gat ctc tac gac atc agg tat gac acc act 307
Glu Phe Trp Leu Ala Asp Asp Leu Tyr Asp Ile Arg Tyr Asp Thr Thr
55 60 65

ttc gac aac ttg ccg ttc acc tat ccc cct ttc ggt gcg ttg gtg ttc 355
Phe Asp Asn Leu Pro Phe Thr Tyr Pro Pro Phe Gly Ala Leu Val Phe
70 75 80 85

acc cca ttg tgg tgg att cat gac ctc ttt ggt ctt ctc gtc acc gaa 403
Thr Pro Leu Trp Trp Ile His Asp Leu Phe Gly Leu Leu Val Thr Glu
90 95 100

cgt gtc ttc gcg cta atc acg ctg ctc acc acc tac gct gtg gca gtt 451
Arg Val Phe Ala Leu Ile Thr Leu Leu Thr Thr Tyr Ala Val Ala Val
105 110 115

ttc ctg ctc cgc ctg gcc ggc gtg cgc gat cgt gtg tgg gaa ttc gtc 499
Phe Leu Leu Arg Leu Ala Gly Val Arg Asp Arg Val Trp Glu Phe Val
120 125 130

gca ttc gca gcc ctg ctc gtg tcc gcg ccg gtg tat ttc aca ctc aat 547
Ala Phe Ala Ala Leu Leu Val Ser Ala Pro Val Tyr Phe Thr Leu Asn
135 140 145

att ggg caa ata aac gtc atg ctc atg gct tta acg ctt ttc gac gtc 595
Ile Gly Gln Ile Asn Val Met Leu Met Ala Leu Thr Leu Phe Asp Val
150 155 160 165

gcc ctc ccc cgc agc acg cgc cat tca ggc gtg ctc aaa tac gtg cca 643
Ala Leu Pro Arg Ser Thr Arg His Ser Gly Val Leu Lys Tyr Val Pro
170 175 180

ctc ggc gta ctc acc ggc att gcc gct gcg atc aaa cta acc cca cta 691

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Leu Gly Val Leu Thr Gly Ile Ala Ala Ala Ile Lys Leu Thr Pro Leu
            185                 190                 195

gtg ttc ggg ctg tat ttc ctc atc ctg tgg gtc gtg act aaa tca cca   739
Val Phe Gly Leu Tyr Phe Leu Ile Leu Trp Val Val Thr Lys Ser Pro
        200                 205                 210

cgc gga ctg ttt gga atg att ggt ggc ttc ctc ggg gca tcc ggg ctt   787
Arg Gly Leu Phe Gly Met Ile Gly Gly Phe Leu Gly Ala Ser Gly Leu
    215                 220                 225

gca att att ttc cga cca tcc att agc atc caa tat ttc acc gac gtg   835
Ala Ile Ile Phe Arg Pro Ser Ile Ser Ile Gln Tyr Phe Thr Asp Val
230                 235                 240                 245

ctg ttt acc gca gaa cgc atc ggc gac ctc cac ttc gca cgc aat gtc   883
Leu Phe Thr Ala Glu Arg Ile Gly Asp Leu His Phe Ala Arg Asn Val
                250                 255                 260

tcc atc cgt gcg gtt ttg gaa cga ctc ccc gaa ctt ggt tcc gca gca   931
Ser Ile Arg Ala Val Leu Glu Arg Leu Pro Glu Leu Gly Ser Ala Ala
            265                 270                 275

tct atc atg tgg ctt gtt gct gtg gcg cta gtg atc atc gca gtc gca   979
Ser Ile Met Trp Leu Val Ala Val Ala Leu Val Ile Ile Ala Val Ala
        280                 285                 290

gtt gct gct tac cga atc ctg cgg acg gat ctc tcc gcg cac aat cgt   1027
Val Ala Ala Tyr Arg Ile Leu Arg Thr Asp Leu Ser Ala His Asn Arg
    295                 300                 305

ctg ctg gct gtt tcc ctc gtg tcg ctc gtt gca ctg ttg tgc tcc ccc   1075
Leu Leu Ala Val Ser Leu Val Ser Leu Val Ala Leu Leu Cys Ser Pro
310                 315                 320                 325

gtc agt tgg tac cac cac tgg gtg tgg ctt ggt ccg tta atc gtc gct   1123
Val Ser Trp Tyr His His Trp Val Trp Leu Gly Pro Leu Ile Val Ala
                330                 335                 340

ctc tgg cta act caa cac cgc tgg ctg gct cta tgg ggc gca ttc gcc   1171
Leu Trp Leu Thr Gln His Arg Trp Leu Ala Leu Trp Gly Ala Phe Ala
            345                 350                 355

gtg aca ttc gga tca ttc cac aat ttc cta ccc tca gaa aac aat atg   1219
Val Thr Phe Gly Ser Phe His Asn Phe Leu Pro Ser Glu Asn Asn Met
        360                 365                 370

gag ctc acc tgg ccg tgg tgg atg cat gtc ctc gca gca cat tat ttg   1267
Glu Leu Thr Trp Pro Trp Trp Met His Val Leu Ala Ala His Tyr Leu
    375                 380                 385

atc ttc tcc gca gtg gtt act gcc gta ttt agt tgt ggg aaa atg ccc   1315
Ile Phe Ser Ala Val Val Thr Ala Val Phe Ser Cys Gly Lys Met Pro
390                 395                 400                 405

caa aaa aca gag ctt tcc cac taatcgatca ggagtatcac atc             1359
Gln Lys Thr Glu Leu Ser His
                410
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<210> 2862

<211> 412
<212> PRT
<213> Corynebacterium glutamicum

<400> 2862

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Val Val Pro Ser Leu Gln Gln Trp Arg Lys Pro Ala Leu Ile Leu Ala
  1               5                  10                  15

Ile Leu Thr Val Leu Gly Val Leu Leu Thr His Trp Phe Ala Trp Pro
             20                  25                  30

Leu Thr Trp Pro Leu Gly Leu Arg Leu Pro Val Asp Val Glu Val Tyr
         35                  40                  45

Trp Gln Gly Ala Arg Glu Phe Trp Leu Ala Asp Asp Leu Tyr Asp Ile
     50                  55                  60

Arg Tyr Asp Thr Thr Phe Asp Asn Leu Pro Phe Thr Tyr Pro Pro Phe
 65                  70                  75                  80

Gly Ala Leu Val Phe Thr Pro Leu Trp Trp Ile His Asp Leu Phe Gly
                 85                  90                  95

Leu Leu Val Thr Glu Arg Val Phe Ala Leu Ile Thr Leu Leu Thr Thr
            100                 105                 110

Tyr Ala Val Ala Val Phe Leu Leu Arg Leu Ala Gly Val Arg Asp Arg
        115                 120                 125

Val Trp Glu Phe Val Ala Phe Ala Ala Leu Leu Val Ser Ala Pro Val
    130                 135                 140

Tyr Phe Thr Leu Asn Ile Gly Gln Ile Asn Val Met Leu Met Ala Leu
145                 150                 155                 160

Thr Leu Phe Asp Val Ala Leu Pro Arg Ser Thr Arg His Ser Gly Val
                165                 170                 175

Leu Lys Tyr Val Pro Leu Gly Val Leu Thr Gly Ile Ala Ala Ala Ile
            180                 185                 190

Lys Leu Thr Pro Leu Val Phe Gly Leu Tyr Phe Leu Ile Leu Trp Val
        195                 200                 205

Val Thr Lys Ser Pro Arg Gly Leu Phe Gly Met Ile Gly Gly Phe Leu
    210                 215                 220

Gly Ala Ser Gly Leu Ala Ile Ile Phe Arg Pro Ser Ile Ser Ile Gln
225                 230                 235                 240

Tyr Phe Thr Asp Val Leu Phe Thr Ala Glu Arg Ile Gly Asp Leu His
                245                 250                 255

Phe Ala Arg Asn Val Ser Ile Arg Ala Val Leu Glu Arg Leu Pro Glu
            260                 265                 270

Leu Gly Ser Ala Ala Ser Ile Met Trp Leu Val Ala Val Ala Leu Val
        275                 280                 285

Ile Ile Ala Val Ala Val Ala Ala Tyr Arg Ile Leu Arg Thr Asp Leu
    290                 295                 300
```

```
Ser Ala His Asn Arg Leu Leu Ala Val Ser Leu Val Ser Leu Val Ala
305                 310                 315                 320

Leu Leu Cys Ser Pro Val Ser Trp Tyr His His Trp Val Trp Leu Gly
                325                 330                 335

Pro Leu Ile Val Ala Leu Trp Leu Thr Gln His Arg Trp Leu Ala Leu
            340                 345                 350

Trp Gly Ala Phe Ala Val Thr Phe Gly Ser Phe His Asn Phe Leu Pro
        355                 360                 365

Ser Glu Asn Asn Met Glu Leu Thr Trp Pro Trp Trp Met His Val Leu
    370                 375                 380

Ala Ala His Tyr Leu Ile Phe Ser Ala Val Val Thr Ala Val Phe Ser
385                 390                 395                 400

Cys Gly Lys Met Pro Gln Lys Thr Glu Leu Ser His
                405                 410
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US 20050287652 A1 20051229

<210> 2863
<211> 1423
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1408)
<223> RXA02701

<400> 2863

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cccactaatc gatcaggagt atcacatctc catgatttaa gattaaaact ttgtctaaac 60

acgaacggtg ttttcatgtt taagaaaagg actcctggtt ttg acg aac ccc cag   115
                                              Leu Thr Asn Pro Gln
                                                1               5

aca gca cat gct gcc gcg tct gac tcc gca tcc cag aag gag gct cct   163
Thr Ala His Ala Ala Ala Ser Asp Ser Ala Ser Gln Lys Glu Ala Pro
                10                  15                  20

aat cct tca ctc tcc atc act gta ggt att aaa gat ctg ctg ggg ctg   211
Asn Pro Ser Leu Ser Ile Thr Val Gly Ile Lys Asp Leu Leu Gly Leu
            25                  30                  35

ctt tca gtt ctt ggc att gca gcg ggg ctg ata gcc aac aag att ctc   259
Leu Ser Val Leu Gly Ile Ala Ala Gly Leu Ile Ala Asn Lys Ile Leu
        40                  45                  50

atc gaa cgc tac aac tgg cgc atc gat gcc gca gtt tac cgc gaa ggc   307
Ile Glu Arg Tyr Asn Trp Arg Ile Asp Ala Ala Val Tyr Arg Glu Gly
    55                  60                  65

gcg tta gcg ctg gtc aac ggg gaa tca ctg tac gcg cag ccg ttt gat   355
Ala Leu Ala Leu Val Asn Gly Glu Ser Leu Tyr Ala Gln Pro Phe Asp
70                  75                  80                  85

atg ggt gat att tca cta ccc ttt atc tac cca ccg att ggt gcc atc   403
```

```
Met Gly Asp Ile Ser Leu Pro Phe Ile Tyr Pro Pro Ile Gly Ala Ile
                 90                  95                 100

ctg ttt gcg cct tgg ggg tac ttt gat ttc atc aca gtt gaa ctt gcg   451
Leu Phe Ala Pro Trp Gly Tyr Phe Asp Phe Ile Thr Val Glu Leu Ala
            105                 110                 115

gga aac ctt gtt gtc ata ggc tca tcc ctg ctg tta tta ctg tgc ctg   499
Gly Asn Leu Val Val Ile Gly Ser Ser Leu Leu Leu Leu Leu Cys Leu
        120                 125                 130

tat ctt gtc acc aac gct gtt ctt agc ggt cga gac aag ctg ttg gcc   547
Tyr Leu Val Thr Asn Ala Val Leu Ser Gly Arg Asp Lys Leu Leu Ala
    135                 140                 145

ttc acc atc gct gcg att tcc tgg ccg atc gct ctc ttt gca gag cca   595
Phe Thr Ile Ala Ala Ile Ser Trp Pro Ile Ala Leu Phe Ala Glu Pro
150                 155                 160                 165

gtg ttt ttg aac gct gac ttg ggc caa atc aac att ttg atc atg gct   643
Val Phe Leu Asn Ala Asp Leu Gly Gln Ile Asn Ile Leu Ile Met Ala
                170                 175                 180

ttg gtt gtc atg gac ctg ctt ccg att aag cgc aga atc ccc cga ggt   691
Leu Val Val Met Asp Leu Leu Pro Ile Lys Arg Arg Ile Pro Arg Gly
            185                 190                 195

gtc ctg att ggc ctt gca gcc gcc atc aaa atc act ccg ctg gcc atg   739
Val Leu Ile Gly Leu Ala Ala Ala Ile Lys Ile Thr Pro Leu Ala Met
        200                 205                 210

ctg ttg tat ttc ctg gtg aag aag gat ttc cgc gga atc atc aat gcg   787
Leu Leu Tyr Phe Leu Val Lys Lys Asp Phe Arg Gly Ile Ile Asn Ala
    215                 220                 225

gtg atc tca cta ctt gcc ttc act gct atc ggt gct gtg ctc gca tgg   835
Val Ile Ser Leu Leu Ala Phe Thr Ala Ile Gly Ala Val Leu Ala Trp
230                 235                 240                 245

gaa aac acc aaa gag ttc ttc tct tca acc ctt ctc aac tta agt gct   883
Glu Asn Thr Lys Glu Phe Phe Ser Ser Thr Leu Leu Asn Leu Ser Ala
                250                 255                 260

gaa ggc gat tca ggc gta gac acc acg ttc caa tcc aac agc tcg att   931
Glu Gly Asp Ser Gly Val Asp Thr Thr Phe Gln Ser Asn Ser Ser Ile
            265                 270                 275

cag gcc atg ctg tat cgc tgg tgg acc tca aag gca gat gcc gaa gca   979
Gln Ala Met Leu Tyr Arg Trp Trp Thr Ser Lys Ala Asp Ala Glu Ala
        280                 285                 290

tcc tca ctg ccc acc atc ttg tgg atc gta ctg tcc ctg att gct gtg   1027
Ser Ser Leu Pro Thr Ile Leu Trp Ile Val Leu Ser Leu Ile Ala Val
    295                 300                 305

gcg gcc gtt gcc tac cta atg cac caa ctc ttc tcc aga gga ttg cac   1075
Ala Ala Val Ala Tyr Leu Met His Gln Leu Phe Ser Arg Gly Leu His
310                 315                 320                 325

gtt gag gca gtc atg gtt aac gcc atg ctc atg cta ctt atc tcc ccc   1123
Val Glu Ala Val Met Val Asn Ala Met Leu Met Leu Leu Ile Ser Pro
```

```
                330                 335                 340

atc tca tgg tct cac cac tgg gtg tgg cta ccg ctg tgg gct gtg gtg   1171
Ile Ser Trp Ser His His Trp Val Trp Leu Pro Leu Trp Ala Val Val
            345                 350                 355

ttc ttc gtt cga tac cgc cag cac cgc tct cac ccg aag ttc ttg ttg   1219
Phe Phe Val Arg Tyr Arg Gln His Arg Ser His Pro Lys Phe Leu Leu
        360                 365                 370

tgg agc gga gtt atc ttg agc gtc atg ctg ctg atg ctg cca cca aaa   1267
Trp Ser Gly Val Ile Leu Ser Val Met Leu Leu Met Leu Pro Pro Lys
    375                 380                 385

tgg tgg ttt ggc cgc gat ggc gtc aac gtc ttc gaa ctg aat ttc tgg   1315
Trp Trp Phe Gly Arg Asp Gly Val Asn Val Phe Glu Leu Asn Phe Trp
390                 395                 400                 405

gag aaa cta ctc atc tct gac tgg acg tgg ctc tcc atc ggg ctc atg   1363
Glu Lys Leu Leu Ile Ser Asp Trp Thr Trp Leu Ser Ile Gly Leu Met
                410                 415                 420

atc acc ttg ggt ctt ggg ctg aaa gca ttt ccc aaa ata tcc aaa       1408
Ile Thr Leu Gly Leu Gly Leu Lys Ala Phe Pro Lys Ile Ser Lys
            425                 430                 435

tagataaagg tgtgg                                                 1423


<210> 2864
<211> 436
<212> PRT
<213> Corynebacterium glutamicum

<400> 2864
Leu Thr Asn Pro Gln Thr Ala His Ala Ala Ala Ser Asp Ser Ala Ser
  1               5                  10                  15

Gln Lys Glu Ala Pro Asn Pro Ser Leu Ser Ile Thr Val Gly Ile Lys
             20                  25                  30

Asp Leu Leu Gly Leu Leu Ser Val Leu Gly Ile Ala Ala Gly Leu Ile
         35                  40                  45

Ala Asn Lys Ile Leu Ile Glu Arg Tyr Asn Trp Arg Ile Asp Ala Ala
     50                  55                  60

Val Tyr Arg Glu Gly Ala Leu Ala Leu Val Asn Gly Glu Ser Leu Tyr
 65                  70                  75                  80

Ala Gln Pro Phe Asp Met Gly Asp Ile Ser Leu Pro Phe Ile Tyr Pro
                 85                  90                  95

Pro Ile Gly Ala Ile Leu Phe Ala Pro Trp Gly Tyr Phe Asp Phe Ile
            100                 105                 110

Thr Val Glu Leu Ala Gly Asn Leu Val Val Ile Gly Ser Ser Leu Leu
        115                 120                 125

Leu Leu Leu Cys Leu Tyr Leu Val Thr Asn Ala Val Leu Ser Gly Arg
    130                 135                 140
```

```
Asp Lys Leu Leu Ala Phe Thr Ile Ala Ala Ile Ser Trp Pro Ile Ala
145                 150                 155                 160

Leu Phe Ala Glu Pro Val Phe Leu Asn Ala Asp Leu Gly Gln Ile Asn
                165                 170                 175

Ile Leu Ile Met Ala Leu Val Val Met Asp Leu Leu Pro Ile Lys Arg
            180                 185                 190

Arg Ile Pro Arg Gly Val Leu Ile Gly Leu Ala Ala Ala Ile Lys Ile
        195                 200                 205

Thr Pro Leu Ala Met Leu Leu Tyr Phe Leu Val Lys Lys Asp Phe Arg
    210                 215                 220

Gly Ile Ile Asn Ala Val Ile Ser Leu Leu Ala Phe Thr Ala Ile Gly
225                 230                 235                 240

Ala Val Leu Ala Trp Glu Asn Thr Lys Glu Phe Phe Ser Ser Thr Leu
                245                 250                 255

Leu Asn Leu Ser Ala Glu Gly Asp Ser Gly Val Asp Thr Thr Phe Gln
            260                 265                 270

Ser Asn Ser Ser Ile Gln Ala Met Leu Tyr Arg Trp Trp Thr Ser Lys
        275                 280                 285

Ala Asp Ala Glu Ala Ser Ser Leu Pro Thr Ile Leu Trp Ile Val Leu
    290                 295                 300

Ser Leu Ile Ala Val Ala Ala Val Ala Tyr Leu Met His Gln Leu Phe
305                 310                 315                 320

Ser Arg Gly Leu His Val Glu Ala Val Met Val Asn Ala Met Leu Met
                325                 330                 335

Leu Leu Ile Ser Pro Ile Ser Trp Ser His His Trp Val Trp Leu Pro
            340                 345                 350

Leu Trp Ala Val Val Phe Phe Val Arg Tyr Arg Gln His Arg Ser His
        355                 360                 365

Pro Lys Phe Leu Leu Trp Ser Gly Val Ile Leu Ser Val Met Leu Leu
    370                 375                 380

Met Leu Pro Pro Lys Trp Trp Phe Gly Arg Asp Gly Val Asn Val Phe
385                 390                 395                 400

Glu Leu Asn Phe Trp Glu Lys Leu Leu Ile Ser Asp Trp Thr Trp Leu
                405                 410                 415

Ser Ile Gly Leu Met Ile Thr Leu Gly Leu Gly Leu Lys Ala Phe Pro
            420                 425                 430

Lys Ile Ser Lys
        435
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<210> 2865
<211> 918

<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(895)
<223> RXA02712

<400> 2865
ctgaaacggc ttcggaagct gaaattgaag aaaacccacg tgccgcacct gtgaaggtgc 60

gcgcaatcga aagaatcggc aacaactcag gagacctctc atg acc atg aca aat 115
Met Thr Met Thr Asn
1 5

ggc tcc cgc aca gag tcg gga aag att cgc gat cga cgt gtc gct gac 163
Gly Ser Arg Thr Glu Ser Gly Lys Ile Arg Asp Arg Arg Val Ala Asp
10 15 20

gct gat cca cgg tat ggc cgt cgc gtc tcg gtg agt agg gat ttc tcc 211
Ala Asp Pro Arg Tyr Gly Arg Arg Val Ser Val Ser Arg Asp Phe Ser
25 30 35

aca gcg gaa gct tcg ggg agg ggc gcg tcg ata agc acg caa cct cgt 259
Thr Ala Glu Ala Ser Gly Arg Gly Ala Ser Ile Ser Thr Gln Pro Arg
40 45 50

cgt gac atg gcg ccg gaa agg cgc cac aca acc cgg gcc cta gtg aac 307
Arg Asp Met Ala Pro Glu Arg Arg His Thr Thr Arg Ala Leu Val Asn
55 60 65

cct ggc gtg caa cca acg cgt aag cgt ttg atg cag cac aag ctg ggc 355
Pro Gly Val Gln Pro Thr Arg Lys Arg Leu Met Gln His Lys Leu Gly
70 75 80 85

tct cag cag gtt atg tcg gtg cgt ggt cgc cgc gtt gag gca aaa cgt 403
Ser Gln Gln Val Met Ser Val Arg Gly Arg Arg Val Glu Ala Lys Arg
90 95 100

gct gat cct aag gtg atc cag ctg tct gtg ctg gtg gtt atc ctg ctg 451
Ala Asp Pro Lys Val Ile Gln Leu Ser Val Leu Val Val Ile Leu Leu
105 110 115

tgc gtt ggt gtt ggc gcg acc atg ggt ctg tcc gga acg tct aca cag 499
Cys Val Gly Val Gly Ala Thr Met Gly Leu Ser Gly Thr Ser Thr Gln
120 125 130

cag act ttc cag ttg cag gaa ctt cag gca act gaa acg gat ttg agc 547
Gln Thr Phe Gln Leu Gln Glu Leu Gln Ala Thr Glu Thr Asp Leu Ser
135 140 145

aat cgc att gag tcg ctc aac cga gat gtg gaa gat gct cgc tca gca 595
Asn Arg Ile Glu Ser Leu Asn Arg Asp Val Glu Asp Ala Arg Ser Ala
150 155 160 165

gca acc ttg gca gcg aat gct acg gag atg ggc ttg gta tcc cca gtg 643
Ala Thr Leu Ala Ala Asn Ala Thr Glu Met Gly Leu Val Ser Pro Val
170 175 180

gaa cct ggc gtg ctc gca gtg cag gaa aac ggt gat gtt gtg gag gag 691
Glu Pro Gly Val Leu Ala Val Gln Glu Asn Gly Asp Val Val Glu Glu

```
            185                 190                 195

cgc gaa gca aat cca gag aca cgc cct ata gtt gac atc aat gga caa   739
Arg Glu Ala Asn Pro Glu Thr Arg Pro Ile Val Asp Ile Asn Gly Gln
        200                 205                 210

cag acc cga cca aat cgg gca tca agc aac cct gac gag act aac gca   787
Gln Thr Arg Pro Asn Arg Ala Ser Ser Asn Pro Asp Glu Thr Asn Ala
    215                 220                 225

gtg act gaa aac ctc cag gcg att cca caa gaa gca gca gct ccg ccg   835
Val Thr Glu Asn Leu Gln Ala Ile Pro Gln Glu Ala Ala Ala Pro Pro
230                 235                 240                 245

tat cag acc aac act gtt cct tat gct gca acc acc gga caa gca ggt   883
Tyr Gln Thr Asn Thr Val Pro Tyr Ala Ala Thr Thr Gly Gln Ala Gly
                250                 255                 260

ggc gca ggg cag tgactttccc cagcaatggc aga                        918
Gly Ala Gly Gln
            265
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Sequence Listing.ST25.txt

<210> 2866
<211> 265
<212> PRT
<213> Corynebacterium glutamicum

<400> 2866

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Met Thr Met Thr Asn Gly Ser Arg Thr Glu Ser Gly Lys Ile Arg Asp
  1               5                  10                  15

Arg Arg Val Ala Asp Ala Asp Pro Arg Tyr Gly Arg Arg Val Ser Val
             20                  25                  30

Ser Arg Asp Phe Ser Thr Ala Glu Ala Ser Gly Arg Gly Ala Ser Ile
         35                  40                  45

Ser Thr Gln Pro Arg Arg Asp Met Ala Pro Glu Arg Arg His Thr Thr
     50                  55                  60

Arg Ala Leu Val Asn Pro Gly Val Gln Pro Thr Arg Lys Arg Leu Met
 65                  70                  75                  80

Gln His Lys Leu Gly Ser Gln Gln Val Met Ser Val Arg Gly Arg Arg
                 85                  90                  95

Val Glu Ala Lys Arg Ala Asp Pro Lys Val Ile Gln Leu Ser Val Leu
            100                 105                 110

Val Val Ile Leu Leu Cys Val Gly Val Gly Ala Thr Met Gly Leu Ser
        115                 120                 125

Gly Thr Ser Thr Gln Gln Thr Phe Gln Leu Gln Glu Leu Gln Ala Thr
    130                 135                 140

Glu Thr Asp Leu Ser Asn Arg Ile Glu Ser Leu Asn Arg Asp Val Glu
145                 150                 155                 160

Asp Ala Arg Ser Ala Ala Thr Leu Ala Ala Asn Ala Thr Glu Met Gly
                165                 170                 175
```

```
Leu Val Ser Pro Val Glu Pro Gly Val Leu Ala Val Gln Glu Asn Gly
            180                 185                 190

Asp Val Val Glu Glu Arg Glu Ala Asn Pro Glu Thr Arg Pro Ile Val
        195                 200                 205

Asp Ile Asn Gly Gln Gln Thr Arg Pro Asn Arg Ala Ser Ser Asn Pro
    210                 215                 220

Asp Glu Thr Asn Ala Val Thr Glu Asn Leu Gln Ala Ile Pro Gln Glu
225                 230                 235                 240

Ala Ala Ala Pro Pro Tyr Gln Thr Asn Thr Val Pro Tyr Ala Ala Thr
                245                 250                 255

Thr Gly Gln Ala Gly Gly Ala Gly Gln
            260                 265


<210> 2867
<211> 552
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(529)
<223> RXA02714

<400> 2867
cgcggtggtc ttgcatgaga ggccactacg caccctcaga gacaaactga atggttggtt 60

ctgtttatgc cactgagttg ctgggaaggg gacttcaagg atg ttc ctt ggt acc   115
                                            Met Phe Leu Gly Thr
                                              1               5

tat acc ccg aaa ctc gat gac aaa ggc agg ctg act ctt cca gca aag   163
Tyr Thr Pro Lys Leu Asp Asp Lys Gly Arg Leu Thr Leu Pro Ala Lys
                10                  15                  20

ttc cgt gag gac ctt gcg ggg gga ttg atg gtc act aaa ggt caa gac   211
Phe Arg Glu Asp Leu Ala Gly Gly Leu Met Val Thr Lys Gly Gln Asp
            25                  30                  35

cac agt ctc gcg gtt tat ccg aag gaa gaa ttt gca gca agg gct cgc   259
His Ser Leu Ala Val Tyr Pro Lys Glu Glu Phe Ala Ala Arg Ala Arg
        40                  45                  50

aag gca gct gca gtt tct agg aca aac cct gag gct cgt gcg ttt atc   307
Lys Ala Ala Ala Val Ser Arg Thr Asn Pro Glu Ala Arg Ala Phe Ile
    55                  60                  65

cga aac ctt gca gca agc gcg gat gaa caa cga ccc gac ggc cag ggg   355
Arg Asn Leu Ala Ala Ser Ala Asp Glu Gln Arg Pro Asp Gly Gln Gly
70                  75                  80                  85

cgc atc acc ctt tcg gca gcg cac cgc aca tat gcg ggg ctg aca aaa   403
Arg Ile Thr Leu Ser Ala Ala His Arg Thr Tyr Ala Gly Leu Thr Lys
                90                  95                  100
```

```
gag tgt gtc gtt atc ggt tcg gtg gat ttt ctg gag att tgg gac gct   451
Glu Cys Val Val Ile Gly Ser Val Asp Phe Leu Glu Ile Trp Asp Ala
            105                 110                 115

caa gcc tgg gcc gcg tat cag gaa gag acg gag gct gcc ttc tca gca   499
Gln Ala Trp Ala Ala Tyr Gln Glu Glu Thr Glu Ala Ala Phe Ser Ala
        120                 125                 130

gct gaa gat gac gtc ctt gga gga ttg ctc tgatagttgg gcaatgcttc     549
Ala Glu Asp Asp Val Leu Gly Gly Leu Leu
    135                 140

gaa                                                               552


<210> 2868
<211> 143
<212> PRT
<213> Corynebacterium glutamicum

<400> 2868
Met Phe Leu Gly Thr Tyr Thr Pro Lys Leu Asp Asp Lys Gly Arg Leu
  1               5                  10                  15

Thr Leu Pro Ala Lys Phe Arg Glu Asp Leu Ala Gly Gly Leu Met Val
             20                  25                  30

Thr Lys Gly Gln Asp His Ser Leu Ala Val Tyr Pro Lys Glu Glu Phe
         35                  40                  45

Ala Ala Arg Ala Arg Lys Ala Ala Ala Val Ser Arg Thr Asn Pro Glu
     50                  55                  60

Ala Arg Ala Phe Ile Arg Asn Leu Ala Ala Ser Ala Asp Glu Gln Arg
 65                  70                  75                  80

Pro Asp Gly Gln Gly Arg Ile Thr Leu Ser Ala Ala His Arg Thr Tyr
                 85                  90                  95

Ala Gly Leu Thr Lys Glu Cys Val Val Ile Gly Ser Val Asp Phe Leu
            100                 105                 110

Glu Ile Trp Asp Ala Gln Ala Trp Ala Ala Tyr Gln Glu Glu Thr Glu
        115                 120                 125

Ala Ala Phe Ser Ala Ala Glu Asp Asp Val Leu Gly Gly Leu Leu
    130                 135                 140


<210> 2869
<211> 513
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(490)
<223> RXA02715

<400> 2869
gtttttgtcg ttattggcat aacggggaac attctggata ttctgggcgt taataaggca 60
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tagaagaaaa aatgtctcta ctaaccaccg ggaggacatc gtg tcg ctt tca gag   115
                                              Val Ser Leu Ser Glu
                                                1               5

cag gag caa cgc gca ctg cgc gaa att gag caa gcg ctc atg gca gat   163
Gln Glu Gln Arg Ala Leu Arg Glu Ile Glu Gln Ala Leu Met Ala Asp
                10                  15                  20

gat ccg aaa ttt gga aaa gcg gtt gca agt aac aat ggc cta gca ggc   211
Asp Pro Lys Phe Gly Lys Ala Val Ala Ser Asn Asn Gly Leu Ala Gly
            25                  30                  35

ggt ggg ttt acc ctt cgg gga atc gca ctt ttc gta ctc gga ctt gtc   259
Gly Gly Phe Thr Leu Arg Gly Ile Ala Leu Phe Val Leu Gly Leu Val
        40                  45                  50

ctt ctt gtt gcc ggc gtc gca tta agc cag caa aca ttg tgg ttc gtt   307
Leu Leu Val Ala Gly Val Ala Leu Ser Gln Gln Thr Leu Trp Phe Val
    55                  60                  65

gcg ctc gga att atc gga ttc tta gtc atg ttc gga tcg gga gtg tgg   355
Ala Leu Gly Ile Ile Gly Phe Leu Val Met Phe Gly Ser Gly Val Trp
70                  75                  80                  85

atg ctg cgc ggg ggc ggc tcc aac aaa atc tcc gtc aca tcc cgc act   403
Met Leu Arg Gly Gly Gly Ser Asn Lys Ile Ser Val Thr Ser Arg Thr
                90                  95                  100

tcc aat gcg aag aat cgc caa cag ggc aat tcc acc att ggg gac aaa   451
Ser Asn Ala Lys Asn Arg Gln Gln Gly Asn Ser Thr Ile Gly Asp Lys
            105                 110                 115

atg gaa gaa aac ttc cgt cga cga ttc gag ggc aat aag taagaagtaa    500
Met Glu Glu Asn Phe Arg Arg Arg Phe Glu Gly Asn Lys
        120                 125                 130

ctgaataagt ctt                                                   513


<210> 2870
<211> 130
<212> PRT
<213> Corynebacterium glutamicum

<400> 2870
Val Ser Leu Ser Glu Gln Glu Gln Arg Ala Leu Arg Glu Ile Glu Gln
  1               5                  10                  15

Ala Leu Met Ala Asp Asp Pro Lys Phe Gly Lys Ala Val Ala Ser Asn
            20                  25                  30

Asn Gly Leu Ala Gly Gly Gly Phe Thr Leu Arg Gly Ile Ala Leu Phe
        35                  40                  45

Val Leu Gly Leu Val Leu Leu Val Ala Gly Val Ala Leu Ser Gln Gln
    50                  55                  60

Thr Leu Trp Phe Val Ala Leu Gly Ile Ile Gly Phe Leu Val Met Phe
65                  70                  75                  80
```

```
Gly Ser Gly Val Trp Met Leu Arg Gly Gly Gly Ser Asn Lys Ile Ser
                85                  90                  95

Val Thr Ser Arg Thr Ser Asn Ala Lys Asn Arg Gln Gln Gly Asn Ser
            100                 105                 110

Thr Ile Gly Asp Lys Met Glu Glu Asn Phe Arg Arg Arg Phe Glu Gly
        115                 120                 125

Asn Lys
    130


<210> 2871
<211> 861
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(838)
<223> RXA02721

<400> 2871
ccgtgatgat cgtcgtgacg atcgccgcga tgaccgcgga gacgacctgg atgtacccag 60

cttcctccag taattaagaa ggagaataga cttatccact atg gat agt ctt gac   115
                                            Met Asp Ser Leu Asp
                                              1               5

ccc cgc aac cgc ccc gtc cgc aag gtc ttc acg acc cgt gcc ggc ggg   163
Pro Arg Asn Arg Pro Val Arg Lys Val Phe Thr Thr Arg Ala Gly Gly
                10                  15                  20

gtt tcg cag tcc ccg tat gct tcc ttc aac ctt ggt gat cac gtc ggc   211
Val Ser Gln Ser Pro Tyr Ala Ser Phe Asn Leu Gly Asp His Val Gly
            25                  30                  35

gac gat cct caa gct gtg gca tcc aac cgc aat cgc ttg gct gac atc   259
Asp Asp Pro Gln Ala Val Ala Ser Asn Arg Asn Arg Leu Ala Asp Ile
        40                  45                  50

atc ggt ttg tcc cca gac aag gtg gtg tac atg gag caa att cat tcc   307
Ile Gly Leu Ser Pro Asp Lys Val Val Tyr Met Glu Gln Ile His Ser
    55                  60                  65

aat acc gtc aca gtc att gat gaa gcc cca gcg gat ggc cag gct gta   355
Asn Thr Val Thr Val Ile Asp Glu Ala Pro Ala Asp Gly Gln Ala Val
70                  75                  80                  85

gag gcc acc gat gcg cta gtg acc acg caa cga ggg cta gcg ctg gcc   403
Glu Ala Thr Asp Ala Leu Val Thr Thr Gln Arg Gly Leu Ala Leu Ala
                90                  95                  100

gtt ttg gtt gct gat tgc gtg cca gtg ctg ctg tca gac acc gac gct   451
Val Leu Val Ala Asp Cys Val Pro Val Leu Leu Ser Asp Thr Asp Ala
            105                 110                 115

ggc gtg att gcg gca gtg cat gca ggc cgc atg gga gcc cgc aat ggc   499
Gly Val Ile Ala Ala Val His Ala Gly Arg Met Gly Ala Arg Asn Gly
        120                 125                 130
```

```
atc gta gct aaa acc att gcg aag atg gag gag ctc ggc gcg aaa ccc   547
Ile Val Ala Lys Thr Ile Ala Lys Met Glu Glu Leu Gly Ala Lys Pro
    135                 140                 145

agc cgc att cat gcg ctc atg ggt gca gcg gca tcg ggt gcg aac tac   595
Ser Arg Ile His Ala Leu Met Gly Ala Ala Ala Ser Gly Ala Asn Tyr
150                 155                 160                 165

gag gtc cca gag gcc atg gcg cgc gat gtg gaa gcc aaa ctt cca ggt   643
Glu Val Pro Glu Ala Met Ala Arg Asp Val Glu Ala Lys Leu Pro Gly
                170                 175                 180

tcc att gcg cgt acg aca aaa ggc acc aca gga ctg gac atc cgc gca   691
Ser Ile Ala Arg Thr Thr Lys Gly Thr Thr Gly Leu Asp Ile Arg Ala
            185                 190                 195

ggg ctg ctg cgt caa atg ctc agc ctg ggt gtg caa atg att gat tct   739
Gly Leu Leu Arg Gln Met Leu Ser Leu Gly Val Gln Met Ile Asp Ser
        200                 205                 210

gat cca cgc tgc acc atc gaa gac gaa gat ctg ttt tct tac cgc cgc   787
Asp Pro Arg Cys Thr Ile Glu Asp Glu Asp Leu Phe Ser Tyr Arg Arg
    215                 220                 225

gaa ggc acg aca ggc cgc cag gcc ggc gtg gtg tgg ctg cca aag gag   835
Glu Gly Thr Thr Gly Arg Gln Ala Gly Val Val Trp Leu Pro Lys Glu
230                 235                 240                 245

gca taaattggag cgccgcgaag agc                                    861
Ala
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<210> 2872
<211> 246
<212> PRT
<213> Corynebacterium glutamicum

<400> 2872

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Met Asp Ser Leu Asp Pro Arg Asn Arg Pro Val Arg Lys Val Phe Thr
  1               5                  10                  15

Thr Arg Ala Gly Gly Val Ser Gln Ser Pro Tyr Ala Ser Phe Asn Leu
             20                  25                  30

Gly Asp His Val Gly Asp Asp Pro Gln Ala Val Ala Ser Asn Arg Asn
         35                  40                  45

Arg Leu Ala Asp Ile Ile Gly Leu Ser Pro Asp Lys Val Val Tyr Met
     50                  55                  60

Glu Gln Ile His Ser Asn Thr Val Thr Val Ile Asp Glu Ala Pro Ala
 65                  70                  75                  80

Asp Gly Gln Ala Val Glu Ala Thr Asp Ala Leu Val Thr Thr Gln Arg
                 85                  90                  95

Gly Leu Ala Leu Ala Val Leu Val Ala Asp Cys Val Pro Val Leu Leu
            100                 105                 110
```

```
Ser Asp Thr Asp Ala Gly Val Ile Ala Ala Val His Ala Gly Arg Met
        115                 120                 125

Gly Ala Arg Asn Gly Ile Val Ala Lys Thr Ile Ala Lys Met Glu Glu
    130                 135                 140

Leu Gly Ala Lys Pro Ser Arg Ile His Ala Leu Met Gly Ala Ala Ala
145                 150                 155                 160

Ser Gly Ala Asn Tyr Glu Val Pro Glu Ala Met Ala Arg Asp Val Glu
                165                 170                 175

Ala Lys Leu Pro Gly Ser Ile Ala Arg Thr Thr Lys Gly Thr Thr Gly
            180                 185                 190

Leu Asp Ile Arg Ala Gly Leu Leu Arg Gln Met Leu Ser Leu Gly Val
        195                 200                 205

Gln Met Ile Asp Ser Asp Pro Arg Cys Thr Ile Glu Asp Glu Asp Leu
    210                 215                 220

Phe Ser Tyr Arg Arg Glu Gly Thr Thr Gly Arg Gln Ala Gly Val Val
225                 230                 235                 240

Trp Leu Pro Lys Glu Ala
                245
```

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<210> 2873
<211> 735
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(712)
<223> RXA02725

<400> 2873

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gaaagcccgc tgcacatcgg tgtggcgggt tttctcatgc ccagatattg accttgtcac 60

tgtgtcaagg cattgaataa gtgccatgaa cataagtgcc atg gac aac ttc gaa   115
                                              Met Asp Asn Phe Glu
                                                1               5

cat tca aat gca tct atc cgt tta caa gca gcg ttg gcc gca gga act   163
His Ser Asn Ala Ser Ile Arg Leu Gln Ala Ala Leu Ala Ala Gly Thr
                10                  15                  20

gct gag gac acc act gcg atc gat att ctt ttg tac cgc agt ggg gta   211
Ala Glu Asp Thr Thr Ala Ile Asp Ile Leu Leu Tyr Arg Ser Gly Val
            25                  30                  35

gaa gaa gac ttc ttt gtg cgc gac atg ata acg tgg gcg ctc acc cgc   259
Glu Glu Asp Phe Phe Val Arg Asp Met Ile Thr Trp Ala Leu Thr Arg
        40                  45                  50

atg cca gtt gat gac gtg ttt acc tca ctg gtc gct gat ttg gat tct   307
Met Pro Val Asp Asp Val Phe Thr Ser Leu Val Ala Asp Leu Asp Ser
    55                  60                  65
```

```
gag gta cct gat cga cca ttc ggt gca agt caa gca ctc cac aca ctc   355
Glu Val Pro Asp Arg Pro Phe Gly Ala Ser Gln Ala Leu His Thr Leu
 70                  75                  80                  85

tcc aag tta agg gtc gcg cag tcg tgg cag gaa ttg caa gca cgg cct   403
Ser Lys Leu Arg Val Ala Gln Ser Trp Gln Glu Leu Gln Ala Arg Pro
                90                  95                 100

tgg ctt ttg cac cgg gag gac acc gcc caa act gcg tgg cga acc ttt   451
Trp Leu Leu His Arg Glu Asp Thr Ala Gln Thr Ala Trp Arg Thr Phe
            105                 110                 115

gtg gga ctg gtc cca gat gat cag acc gca tgg ttg gcg cac caa ttg   499
Val Gly Leu Val Pro Asp Asp Gln Thr Ala Trp Leu Ala His Gln Leu
        120                 125                 130

ctc caa gaa ttg gat aaa gga acg cct gaa att cag cgg agt tta agt   547
Leu Gln Glu Leu Asp Lys Gly Thr Pro Glu Ile Gln Arg Ser Leu Ser
    135                 140                 145

cgg gcg atg gcg gaa ttg gag ggg agg gag gcg tcg ata agc gtg ctt   595
Arg Ala Met Ala Glu Leu Glu Gly Arg Glu Ala Ser Ile Ser Val Leu
150                 155                 160                 165

cta ggc gct tta acg agc gcg cac gcg gtg gcc acc gcc aag ctc att   643
Leu Gly Ala Leu Thr Ser Ala His Ala Val Ala Thr Ala Lys Leu Ile
                170                 175                 180

gcg gat ccg gac tcc gat ttc atg gct gat ctg gag gaa gcg cgg cgc   691
Ala Asp Pro Asp Ser Asp Phe Met Ala Asp Leu Glu Glu Ala Arg Arg
            185                 190                 195

gtg gat aat atg ggt gca tgc tgatcggtga ggtgtccaag ctc            735
Val Asp Asn Met Gly Ala Cys
        200
```

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<210> 2874
<211> 204
<212> PRT
<213> Corynebacterium glutamicum

<400> 2874

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Met Asp Asn Phe Glu His Ser Asn Ala Ser Ile Arg Leu Gln Ala Ala
  1               5                  10                  15

Leu Ala Ala Gly Thr Ala Glu Asp Thr Thr Ala Ile Asp Ile Leu Leu
             20                  25                  30

Tyr Arg Ser Gly Val Glu Glu Asp Phe Phe Val Arg Asp Met Ile Thr
         35                  40                  45

Trp Ala Leu Thr Arg Met Pro Val Asp Asp Val Phe Thr Ser Leu Val
     50                  55                  60

Ala Asp Leu Asp Ser Glu Val Pro Asp Arg Pro Phe Gly Ala Ser Gln
 65                  70                  75                  80

Ala Leu His Thr Leu Ser Lys Leu Arg Val Ala Gln Ser Trp Gln Glu
                 85                  90                  95
```

```
Leu Gln Ala Arg Pro Trp Leu Leu His Arg Glu Asp Thr Ala Gln Thr
            100                 105                 110

Ala Trp Arg Thr Phe Val Gly Leu Val Pro Asp Asp Gln Thr Ala Trp
        115                 120                 125

Leu Ala His Gln Leu Leu Gln Glu Leu Asp Lys Gly Thr Pro Glu Ile
    130                 135                 140

Gln Arg Ser Leu Ser Arg Ala Met Ala Glu Leu Glu Gly Arg Glu Ala
145                 150                 155                 160

Ser Ile Ser Val Leu Leu Gly Ala Leu Thr Ser Ala His Ala Val Ala
                165                 170                 175

Thr Ala Lys Leu Ile Ala Asp Pro Asp Ser Asp Phe Met Ala Asp Leu
            180                 185                 190

Glu Glu Ala Arg Arg Val Asp Asn Met Gly Ala Cys
        195                 200
```

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<210> 2875
<211> 1035
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1012)
<223> RXA02727

<400> 2875

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gatcagttcc tagatctcgt tgaggacgcc ctcgttcagt tccaagagga aaacgaagac 60

ctaaagcagc aggtcgaaga gctagaggcg caggttgccg gtg gtc ctt ctt ccg   115
                                            Val Val Leu Leu Pro
                                              1               5

ctg cta gtt cct caa ctg cag gtg cag cca cag ttg cag ctt cca agt   163
Leu Leu Val Pro Gln Leu Gln Val Gln Pro Gln Leu Gln Leu Pro Ser
                10                  15                  20

ctg ttg acg agg cag cgc tgc gca agg aaa tca aag aga agc tgc gct   211
Leu Leu Thr Arg Gln Arg Cys Ala Arg Lys Ser Lys Arg Ser Cys Ala
            25                  30                  35

ccg aat acg gca tcc aag ctc gat gat gcc tcc aag gcc gct cag aag   259
Pro Asn Thr Ala Ser Lys Leu Asp Asp Ala Ser Lys Ala Ala Gln Lys
        40                  45                  50

gct caa aac gat gcg aag tcc gct caa gat cag cta cag cgt gca caa   307
Ala Gln Asn Asp Ala Lys Ser Ala Gln Asp Gln Leu Gln Arg Ala Gln
    55                  60                  65

gct gac gca aag gca gct cgc gac gaa gct gaa aag gcc aag gct gaa   355
Ala Asp Ala Lys Ala Ala Arg Asp Glu Ala Glu Lys Ala Lys Ala Glu
70                  75                  80                  85

gct aag tca gca gca tcc tcc agc acc act aag gca gca gcg gtt ggc   403
Ala Lys Ser Ala Ala Ser Ser Ser Thr Thr Lys Ala Ala Ala Val Gly
```

```
                  90                  95                 100

gct gtc ggc gct ggc acc gga gca gca gtt gct aca ggt gct gca aat   451
Ala Val Gly Ala Gly Thr Gly Ala Ala Val Ala Thr Gly Ala Ala Asn
            105                 110                 115

gtg gac acc cac atg cag gca gcg aag gtt ctg gga ctc gca cag gaa   499
Val Asp Thr His Met Gln Ala Ala Lys Val Leu Gly Leu Ala Gln Glu
        120                 125                 130

atg gca gac cgc ctg acc tca gag gct cgc tcc gaa tcc aag tcc atg   547
Met Ala Asp Arg Leu Thr Ser Glu Ala Arg Ser Glu Ser Lys Ser Met
    135                 140                 145

ctg gac gag gct cgc gaa gca gca gag aag cag atc gag gaa gca aac   595
Leu Asp Glu Ala Arg Glu Ala Ala Glu Lys Gln Ile Glu Glu Ala Asn
150                 155                 160                 165

agc acc tcc aac cgc act ctg gaa gat gct cgc gca aac gct gag aag   643
Ser Thr Ser Asn Arg Thr Leu Glu Asp Ala Arg Ala Asn Ala Glu Lys
                170                 175                 180

cag atc gct gaa gcg cag aac cgc gct gac act ctg gtc aac gaa gct   691
Gln Ile Ala Glu Ala Gln Asn Arg Ala Asp Thr Leu Val Asn Glu Ala
            185                 190                 195

gac gct aag gct aag aac ctg gtt tcc gaa gcc gag aag aag tcc gca   739
Asp Ala Lys Ala Lys Asn Leu Val Ser Glu Ala Glu Lys Lys Ser Ala
        200                 205                 210

gcc acc ctg gcc gca tcc acc tct cgt gca gaa gct cag atc cgt caa   787
Ala Thr Leu Ala Ala Ser Thr Ser Arg Ala Glu Ala Gln Ile Arg Gln
    215                 220                 225

gcc gag gac aag gca aac gcc ctc cag gca gac gca gag cgc aag cac   835
Ala Glu Asp Lys Ala Asn Ala Leu Gln Ala Asp Ala Glu Arg Lys His
230                 235                 240                 245

acc gaa acc atg gct gca gtc aag gaa cag cag aat gct ctg gag acc   883
Thr Glu Thr Met Ala Ala Val Lys Glu Gln Gln Asn Ala Leu Glu Thr
                250                 255                 260

cgc atc gcg gaa ctg cag acc ttc gag cgt gag tac cgc acc cgt ctg   931
Arg Ile Ala Glu Leu Gln Thr Phe Glu Arg Glu Tyr Arg Thr Arg Leu
            265                 270                 275

aag tcc ctc ctc gag ggc cag ctg gaa gaa ctc cac gca cgt ggc tcc   979
Lys Ser Leu Leu Glu Gly Gln Leu Glu Glu Leu His Ala Arg Gly Ser
        280                 285                 290

tct gca cca acc aac aac aag cca tct ggt gag taaaaagaaa gattagttat 1032
Ser Ala Pro Thr Asn Asn Lys Pro Ser Gly Glu
    295                 300

ctt                                                               1035


<210> 2876
<211> 304
<212> PRT
<213> Corynebacterium glutamicum
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<400> 2876

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Val Val Leu Leu Pro Leu Leu Val Pro Gln Leu Gln Val Gln Pro Gln
  1               5                  10                  15

Leu Gln Leu Pro Ser Leu Leu Thr Arg Gln Arg Cys Ala Arg Lys Ser
            20                  25                  30

Lys Arg Ser Cys Ala Pro Asn Thr Ala Ser Lys Leu Asp Asp Ala Ser
        35                  40                  45

Lys Ala Ala Gln Lys Ala Gln Asn Asp Ala Lys Ser Ala Gln Asp Gln
    50                  55                  60

Leu Gln Arg Ala Gln Ala Asp Ala Lys Ala Ala Arg Asp Glu Ala Glu
65                  70                  75                  80

Lys Ala Lys Ala Glu Ala Lys Ser Ala Ala Ser Ser Ser Thr Thr Lys
                85                  90                  95

Ala Ala Ala Val Gly Ala Val Gly Ala Gly Thr Gly Ala Ala Val Ala
            100                 105                 110

Thr Gly Ala Ala Asn Val Asp Thr His Met Gln Ala Ala Lys Val Leu
        115                 120                 125

Gly Leu Ala Gln Glu Met Ala Asp Arg Leu Thr Ser Glu Ala Arg Ser
    130                 135                 140

Glu Ser Lys Ser Met Leu Asp Glu Ala Arg Glu Ala Ala Glu Lys Gln
145                 150                 155                 160

Ile Glu Glu Ala Asn Ser Thr Ser Asn Arg Thr Leu Glu Asp Ala Arg
                165                 170                 175

Ala Asn Ala Glu Lys Gln Ile Ala Glu Ala Gln Asn Arg Ala Asp Thr
            180                 185                 190

Leu Val Asn Glu Ala Asp Ala Lys Ala Lys Asn Leu Val Ser Glu Ala
        195                 200                 205

Glu Lys Lys Ser Ala Ala Thr Leu Ala Ala Ser Thr Ser Arg Ala Glu
    210                 215                 220

Ala Gln Ile Arg Gln Ala Glu Asp Lys Ala Asn Ala Leu Gln Ala Asp
225                 230                 235                 240

Ala Glu Arg Lys His Thr Glu Thr Met Ala Ala Val Lys Glu Gln Gln
                245                 250                 255

Asn Ala Leu Glu Thr Arg Ile Ala Glu Leu Gln Thr Phe Glu Arg Glu
            260                 265                 270

Tyr Arg Thr Arg Leu Lys Ser Leu Leu Glu Gly Gln Leu Glu Glu Leu
        275                 280                 285

His Ala Arg Gly Ser Ser Ala Pro Thr Asn Asn Lys Pro Ser Gly Glu
    290                 295                 300
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<210> 2877
<211> 828
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(805)
<223> RXA02735

<400> 2877
gaggagcttc gccacatgga tccagatttg ggctaccagc acgcactatc cggcttgtcc 60

agcgtcaagc tggaaaccgt ctaaggagaa atacaacact atg gtt gat gta gta 115
Met Val Asp Val Val
1 5

cgc gca cgc gat act gaa gat ttg gtt gca cag gct gcc tcc aaa ttc 163
Arg Ala Arg Asp Thr Glu Asp Leu Val Ala Gln Ala Ala Ser Lys Phe
10 15 20

att gag gtt gtt gaa gca gca act gcc aat aat ggc acc gca cag gta 211
Ile Glu Val Val Glu Ala Ala Thr Ala Asn Asn Gly Thr Ala Gln Val
25 30 35

gtg ctc acc ggt ggt ggc gcc ggc atc aag ttg ctg gaa aag ctc agc 259
Val Leu Thr Gly Gly Gly Ala Gly Ile Lys Leu Leu Glu Lys Leu Ser
40 45 50

gtt gat gcg gct gac ctt gcc tgg gat cgc att cat gtg ttc ttc ggc 307
Val Asp Ala Ala Asp Leu Ala Trp Asp Arg Ile His Val Phe Phe Gly
55 60 65

gat gag cgc aat gtc cct gtc agt gat tct gag tcc aat gag ggc cag 355
Asp Glu Arg Asn Val Pro Val Ser Asp Ser Glu Ser Asn Glu Gly Gln
70 75 80 85

gct cgt gag gca ctg ttg tcc aag gtt tct atc cct gaa gcc aac att 403
Ala Arg Glu Ala Leu Leu Ser Lys Val Ser Ile Pro Glu Ala Asn Ile
90 95 100

cac gga tat ggt ctc ggc gac gta gat ctt gca gag gca gcc cgc gct 451
His Gly Tyr Gly Leu Gly Asp Val Asp Leu Ala Glu Ala Ala Arg Ala
105 110 115

tac gaa gct gtg ttg gat gaa ttc gca cca aac ggc ttt gat ctt cac 499
Tyr Glu Ala Val Leu Asp Glu Phe Ala Pro Asn Gly Phe Asp Leu His
120 125 130

ctg ctc ggc atg ggt ggc gaa ggc cat atc aac tcc ctg ttc cct cac 547
Leu Leu Gly Met Gly Gly Glu Gly His Ile Asn Ser Leu Phe Pro His
135 140 145

acc gat gca gtc aag gaa tcc tcc gca aag gtc atc gcg gtg ttt gat 595
Thr Asp Ala Val Lys Glu Ser Ser Ala Lys Val Ile Ala Val Phe Asp
150 155 160 165

tcc cct aag cct cct tca gag cgt gca act cta acc ctt cct gcg gtt 643
Ser Pro Lys Pro Pro Ser Glu Arg Ala Thr Leu Thr Leu Pro Ala Val

```
                170                 175                 180

cac tcc gca aag cgc gtg tgg ttg ctg gtt tct ggt gcg gag aag gct   691
His Ser Ala Lys Arg Val Trp Leu Leu Val Ser Gly Ala Glu Lys Ala
            185                 190                 195

gag gca gct gcg gcg atc gtc aac ggt gag cct gct gtt gag tgg cct   739
Glu Ala Ala Ala Ala Ile Val Asn Gly Glu Pro Ala Val Glu Trp Pro
        200                 205                 210

gct gct gga gct acc gga tct gag gaa acg gta ttg ttc ttg gct gat   787
Ala Ala Gly Ala Thr Gly Ser Glu Glu Thr Val Leu Phe Leu Ala Asp
    215                 220                 225

gat gct gca gga aat ctc taagcagcgc cagctctaac aag                 828
Asp Ala Ala Gly Asn Leu
230                 235
```

<210> 2878
<211> 235
<212> PRT
<213> Corynebacterium glutamicum

<400> 2878

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Met Val Asp Val Val Arg Ala Arg Asp Thr Glu Asp Leu Val Ala Gln
  1               5                  10                  15

Ala Ala Ser Lys Phe Ile Glu Val Val Glu Ala Ala Thr Ala Asn Asn
             20                  25                  30

Gly Thr Ala Gln Val Val Leu Thr Gly Gly Gly Ala Gly Ile Lys Leu
         35                  40                  45

Leu Glu Lys Leu Ser Val Asp Ala Ala Asp Leu Ala Trp Asp Arg Ile
     50                  55                  60

His Val Phe Phe Gly Asp Glu Arg Asn Val Pro Val Ser Asp Ser Glu
 65                  70                  75                  80

Ser Asn Glu Gly Gln Ala Arg Glu Ala Leu Leu Ser Lys Val Ser Ile
                 85                  90                  95

Pro Glu Ala Asn Ile His Gly Tyr Gly Leu Gly Asp Val Asp Leu Ala
            100                 105                 110

Glu Ala Ala Arg Ala Tyr Glu Ala Val Leu Asp Glu Phe Ala Pro Asn
        115                 120                 125

Gly Phe Asp Leu His Leu Leu Gly Met Gly Gly Glu Gly His Ile Asn
    130                 135                 140

Ser Leu Phe Pro His Thr Asp Ala Val Lys Glu Ser Ser Ala Lys Val
145                 150                 155                 160

Ile Ala Val Phe Asp Ser Pro Lys Pro Pro Ser Glu Arg Ala Thr Leu
                165                 170                 175

Thr Leu Pro Ala Val His Ser Ala Lys Arg Val Trp Leu Leu Val Ser
            180                 185                 190
```

```
Gly Ala Glu Lys Ala Glu Ala Ala Ala Ala Ile Val Asn Gly Glu Pro
        195                 200                 205

Ala Val Glu Trp Pro Ala Ala Gly Ala Thr Gly Ser Glu Glu Thr Val
    210                 215                 220

Leu Phe Leu Ala Asp Asp Ala Ala Gly Asn Leu
225                 230                 235


<210> 2879
<211> 1080
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1057)
<223> RXA02736

<400> 2879
cagaggatta cccagcgggt acgtggggtc caaagagcgc tgatgaaatg ctttcccgca 60

acggtcacac ctggcgcagg ccataattta ggggcaaaaa atg atc ttt gaa ctt   115
                                            Met Ile Phe Glu Leu
                                              1               5

ccg gat acc acc acc cag caa att tcc aag acc cta act cga ctg cgt   163
Pro Asp Thr Thr Thr Gln Gln Ile Ser Lys Thr Leu Thr Arg Leu Arg
                 10                  15                  20

gaa tcg ggc acc cag gtc acc acc ggc cga gtg ctc acc ctc atc gtg   211
Glu Ser Gly Thr Gln Val Thr Thr Gly Arg Val Leu Thr Leu Ile Val
             25                  30                  35

gtc act gac tcc gaa agc gat gtc gct gca gtt acc gag tcc acc aat   259
Val Thr Asp Ser Glu Ser Asp Val Ala Ala Val Thr Glu Ser Thr Asn
         40                  45                  50

gaa gcc tcg cgc gag cac cca tct cgc gtg atc att ttg gtg gtt ggc   307
Glu Ala Ser Arg Glu His Pro Ser Arg Val Ile Ile Leu Val Val Gly
     55                  60                  65

gat aaa act gca gaa aac aaa gtt gac gca gaa gtc cgt atc ggt ggc   355
Asp Lys Thr Ala Glu Asn Lys Val Asp Ala Glu Val Arg Ile Gly Gly
 70                  75                  80                  85

gac gct ggt gct tcc gag atg atc atc atg cat ctc aac gga cct gtc   403
Asp Ala Gly Ala Ser Glu Met Ile Ile Met His Leu Asn Gly Pro Val
                 90                  95                 100

gct gac aag ctc cag tat gtc gtc aca cca ctg ttg ctt cct gac acc   451
Ala Asp Lys Leu Gln Tyr Val Val Thr Pro Leu Leu Leu Pro Asp Thr
             105                 110                 115

ccc atc gtt gct tgg tgg cca ggt gaa tca cca aag aat cct tcc cag   499
Pro Ile Val Ala Trp Trp Pro Gly Glu Ser Pro Lys Asn Pro Ser Gln
         120                 125                 130

gac cca att gga cgc atc gca caa cga cgc atc act gat gct ttg tac   547
Asp Pro Ile Gly Arg Ile Ala Gln Arg Arg Ile Thr Asp Ala Leu Tyr
```

```
    135                 140                 145

gac cgt gat gac gca cta gaa gat cgt gtt gag aac tat cac cca ggt   595
Asp Arg Asp Asp Ala Leu Glu Asp Arg Val Glu Asn Tyr His Pro Gly
150                 155                 160                 165

gat acc gac atg acg tgg gcg cgc ctt acc cag tgg cgg gga ctt gtt   643
Asp Thr Asp Met Thr Trp Ala Arg Leu Thr Gln Trp Arg Gly Leu Val
                170                 175                 180

gcc tcc tca ttg gat cac cca cca cac agc gaa atc act tcc gtg agg   691
Ala Ser Ser Leu Asp His Pro Pro His Ser Glu Ile Thr Ser Val Arg
            185                 190                 195

ctg acc ggt gca agc ggc agt acc tcg gtg gat ttg gct gca ggc tgg   739
Leu Thr Gly Ala Ser Gly Ser Thr Ser Val Asp Leu Ala Ala Gly Trp
        200                 205                 210

ttg gcg cgg agg ctg aaa gtg cct gtg atc cgc gag gtg aca gat gct   787
Leu Ala Arg Arg Leu Lys Val Pro Val Ile Arg Glu Val Thr Asp Ala
    215                 220                 225

ccc acc gtg cca acc gat gag ttt ggt act cca ctg ctg gct atc cag   835
Pro Thr Val Pro Thr Asp Glu Phe Gly Thr Pro Leu Leu Ala Ile Gln
230                 235                 240                 245

cgc ctg gag atc gtt cgc acc acc ggc tcg atc atc atc acc atc tat   883
Arg Leu Glu Ile Val Arg Thr Thr Gly Ser Ile Ile Ile Thr Ile Tyr
                250                 255                 260

gac gct cat acc ctt cag gta gag atg ccg gaa tcc ggc aat gcc cca   931
Asp Ala His Thr Leu Gln Val Glu Met Pro Glu Ser Gly Asn Ala Pro
            265                 270                 275

tcg ctg gtg gct att ggt cgt cga agt gag tcc gac tgc ttg tct gag   979
Ser Leu Val Ala Ile Gly Arg Arg Ser Glu Ser Asp Cys Leu Ser Glu
        280                 285                 290

gag ctt cgc cac atg gat cca gat ttg ggc tac cag cac gca cta tcc   1027
Glu Leu Arg His Met Asp Pro Asp Leu Gly Tyr Gln His Ala Leu Ser
    295                 300                 305

ggc ttg tcc agc gtc aag ctg gaa acc gtc taaggagaaa tacaacacta     1077
Gly Leu Ser Ser Val Lys Leu Glu Thr Val
310                 315

tgg                                                               1080


<210> 2880
<211> 319
<212> PRT
<213> Corynebacterium glutamicum

<400> 2880
Met Ile Phe Glu Leu Pro Asp Thr Thr Thr Gln Gln Ile Ser Lys Thr
  1               5                  10                  15

Leu Thr Arg Leu Arg Glu Ser Gly Thr Gln Val Thr Thr Gly Arg Val
             20                  25                  30
```

```
Leu Thr Leu Ile Val Val Thr Asp Ser Glu Ser Asp Val Ala Ala Val
         35                  40                  45

Thr Glu Ser Thr Asn Glu Ala Ser Arg Glu His Pro Ser Arg Val Ile
     50                  55                  60

Ile Leu Val Val Gly Asp Lys Thr Ala Glu Asn Lys Val Asp Ala Glu
 65                  70                  75                  80

Val Arg Ile Gly Gly Asp Ala Gly Ala Ser Glu Met Ile Ile Met His
                 85                  90                  95

Leu Asn Gly Pro Val Ala Asp Lys Leu Gln Tyr Val Val Thr Pro Leu
            100                 105                 110

Leu Leu Pro Asp Thr Pro Ile Val Ala Trp Trp Pro Gly Glu Ser Pro
        115                 120                 125

Lys Asn Pro Ser Gln Asp Pro Ile Gly Arg Ile Ala Gln Arg Arg Ile
    130                 135                 140

Thr Asp Ala Leu Tyr Asp Arg Asp Asp Ala Leu Glu Asp Arg Val Glu
145                 150                 155                 160

Asn Tyr His Pro Gly Asp Thr Asp Met Thr Trp Ala Arg Leu Thr Gln
                165                 170                 175

Trp Arg Gly Leu Val Ala Ser Ser Leu Asp His Pro Pro His Ser Glu
            180                 185                 190

Ile Thr Ser Val Arg Leu Thr Gly Ala Ser Gly Ser Thr Ser Val Asp
        195                 200                 205

Leu Ala Ala Gly Trp Leu Ala Arg Arg Leu Lys Val Pro Val Ile Arg
    210                 215                 220

Glu Val Thr Asp Ala Pro Thr Val Pro Thr Asp Glu Phe Gly Thr Pro
225                 230                 235                 240

Leu Leu Ala Ile Gln Arg Leu Glu Ile Val Arg Thr Thr Gly Ser Ile
                245                 250                 255

Ile Ile Thr Ile Tyr Asp Ala His Thr Leu Gln Val Glu Met Pro Glu
            260                 265                 270

Ser Gly Asn Ala Pro Ser Leu Val Ala Ile Gly Arg Arg Ser Glu Ser
        275                 280                 285

Asp Cys Leu Ser Glu Glu Leu Arg His Met Asp Pro Asp Leu Gly Tyr
    290                 295                 300

Gln His Ala Leu Ser Gly Leu Ser Ser Val Lys Leu Glu Thr Val
305                 310                 315
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<210> 2881
<211> 597
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS
<222> (101)..(574)
<223> RXA02751

<400> 2881
ggtgtcttct tgtcaaataa ccactgttta tagggcaatt ctttggcaat gtacccaact 60

cattacccac ctgctgattc aaagagtaga tttaaatagt gtg ctt ccg att gcc 115
Val Leu Pro Ile Ala
1 5

tcc ggt aac gat gac cgg aat tta atc cgt tat gtc gac ggt ggt cga 163
Ser Gly Asn Asp Asp Arg Asn Leu Ile Arg Tyr Val Asp Gly Gly Arg
10 15 20

ttt gat gaa atc atg ctc acc gga gac ctc act ggc ctg agc agt ttt 211
Phe Asp Glu Ile Met Leu Thr Gly Asp Leu Thr Gly Leu Ser Ser Phe
25 30 35

ctt acc aac gct ggc ccg aac gcc cgg gat gat ttt gat ctc acg gtg 259
Leu Thr Asn Ala Gly Pro Asn Ala Arg Asp Asp Phe Asp Leu Thr Val
40 45 50

ctc atg cgc gct gcc gag gca ggc aac ctc atg gtt gtt gcc cgc ttg 307
Leu Met Arg Ala Ala Glu Ala Gly Asn Leu Met Val Val Ala Arg Leu
55 60 65

tta gat tta ggt gcc aat ccc cga ctc acc aat cct cgt ggt gtc acg 355
Leu Asp Leu Gly Ala Asn Pro Arg Leu Thr Asn Pro Arg Gly Val Thr
70 75 80 85

gcc cta cat atc gca gcg atc gcc ggg gac gat ggc att gtg gaa tgc 403
Ala Leu His Ile Ala Ala Ile Ala Gly Asp Asp Gly Ile Val Glu Cys
90 95 100

ctc att gat gca ggc gct gaa gtc gat gct gta gat gat caa ggt cgc 451
Leu Ile Asp Ala Gly Ala Glu Val Asp Ala Val Asp Asp Gln Gly Arg
105 110 115

act ccc cta tgg aac gca gcg gct cat cat ctg cct gat tct gcg gtg 499
Thr Pro Leu Trp Asn Ala Ala Ala His His Leu Pro Asp Ser Ala Val
120 125 130

gtg gat gtg ctg ctt cgc gca ggt gcg aat gtg aat ctg cgc gat tgc 547
Val Asp Val Leu Leu Arg Ala Gly Ala Asn Val Asn Leu Arg Asp Cys
135 140 145

aat gga gtc agc cca gaa gac atg ctg tagaagcatt ctttagcagg 594
Asn Gly Val Ser Pro Glu Asp Met Leu
150 155

att 597

<210> 2882
<211> 158
<212> PRT
<213> Corynebacterium glutamicum

<400> 2882
Val Leu Pro Ile Ala Ser Gly Asn Asp Asp Arg Asn Leu Ile Arg Tyr

```
  1               5                  10                  15

Val Asp Gly Gly Arg Phe Asp Glu Ile Met Leu Thr Gly Asp Leu Thr
            20                  25                  30

Gly Leu Ser Ser Phe Leu Thr Asn Ala Gly Pro Asn Ala Arg Asp Asp
        35                  40                  45

Phe Asp Leu Thr Val Leu Met Arg Ala Ala Glu Ala Gly Asn Leu Met
    50                  55                  60

Val Val Ala Arg Leu Leu Asp Leu Gly Ala Asn Pro Arg Leu Thr Asn
65                  70                  75                  80

Pro Arg Gly Val Thr Ala Leu His Ile Ala Ala Ile Ala Gly Asp Asp
                85                  90                  95

Gly Ile Val Glu Cys Leu Ile Asp Ala Gly Ala Glu Val Asp Ala Val
            100                 105                 110

Asp Asp Gln Gly Arg Thr Pro Leu Trp Asn Ala Ala Ala His His Leu
        115                 120                 125

Pro Asp Ser Ala Val Val Asp Val Leu Leu Arg Ala Gly Ala Asn Val
    130                 135                 140

Asn Leu Arg Asp Cys Asn Gly Val Ser Pro Glu Asp Met Leu
145                 150                 155


<210> 2883
<211> 1014
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(991)
<223> RXA02756

<400> 2883
cgtgacggtt gttgcaattc cataactaaa cgagctttga ttaacaagtc cttgtattgt 60

gtaaatcgct tattgcacac aattgaaaaa ggacattgtt atg aca agc cct tat   115
                                              Met Thr Ser Pro Tyr
                                                1               5

gga tcc caa tac cca ggc gac gac aac aat aat tgg aac tcc cag ttc   163
Gly Ser Gln Tyr Pro Gly Asp Asp Asn Asn Asn Trp Asn Ser Gln Phe
                10                  15                  20

ggc aac cct tcc ggc gag cag aac tac ggt cag ccc tac ggt gcg cca   211
Gly Asn Pro Ser Gly Glu Gln Asn Tyr Gly Gln Pro Tyr Gly Ala Pro
            25                  30                  35

tat gga cag cct tac ggg cag cca ttt gat caa gga ttc aac gcc tac   259
Tyr Gly Gln Pro Tyr Gly Gln Pro Phe Asp Gln Gly Phe Asn Ala Tyr
        40                  45                  50

agt tct ccc atc cca cct gag gtc cca cag cct tcc atg cag gag gct   307
Ser Ser Pro Ile Pro Pro Glu Val Pro Gln Pro Ser Met Gln Glu Ala
```

```
     55                  60                  65

cag tgg cgc tcc ttt gac ctt gga act gtt ttt ggt cag gca tgg aag   355
Gln Trp Arg Ser Phe Asp Leu Gly Thr Val Phe Gly Gln Ala Trp Lys
 70                  75                  80                  85

ggc ttt acc gca acg tgg cag gca tgg gtg ctg tct gca ctg atc tac   403
Gly Phe Thr Ala Thr Trp Gln Ala Trp Val Leu Ser Ala Leu Ile Tyr
                 90                  95                 100

ttc gcg gtg ttg ctt gtg ctg atg ttt gcg tgg atc ctc ccg atg gtt   451
Phe Ala Val Leu Leu Val Leu Met Phe Ala Trp Ile Leu Pro Met Val
            105                 110                 115

agt gtg ctc gca gcg acc tca tct ggt tct gat tcc gca gct att gca   499
Ser Val Leu Ala Ala Thr Ser Ser Gly Ser Asp Ser Ala Ala Ile Ala
        120                 125                 130

gcg acg ggt ggc acc agc ttc ttc ggg ttc atg ctg atg atc gtc ctg   547
Ala Thr Gly Gly Thr Ser Phe Phe Gly Phe Met Leu Met Ile Val Leu
    135                 140                 145

gca ttc atc agt ttt gtg tac tcc ctt aac tgc tac cgc aac gcg gct   595
Ala Phe Ile Ser Phe Val Tyr Ser Leu Asn Cys Tyr Arg Asn Ala Ala
150                 155                 160                 165

cga gtt gtg cgc ggt gag cag atc acc att cag agt ttc ttc aag atg   643
Arg Val Val Arg Gly Glu Gln Ile Thr Ile Gln Ser Phe Phe Lys Met
                170                 175                 180

aag ggt ctt ggt aag gcg ctc ggt att tac atc ttg atc aat atc gtc   691
Lys Gly Leu Gly Lys Ala Leu Gly Ile Tyr Ile Leu Ile Asn Ile Val
            185                 190                 195

atc ttc atc gga atg atc ttg ctg ctc att cct gga att atc gct gcc   739
Ile Phe Ile Gly Met Ile Leu Leu Leu Ile Pro Gly Ile Ile Ala Ala
        200                 205                 210

gtg gtg ctg atc ttt gct gtt cct gtg gca ttc cag ctg cgc gac gcc   787
Val Val Leu Ile Phe Ala Val Pro Val Ala Phe Gln Leu Arg Asp Ala
    215                 220                 225

tcg atc ggt gat gcg ttt tcc gca agc tgg aag gca gtg tcc aaa aac   835
Ser Ile Gly Asp Ala Phe Ser Ala Ser Trp Lys Ala Val Ser Lys Asn
230                 235                 240                 245

gtt ggt cag gtc att ctc tta gaa ctg gct atc ttc gcg ttg agc ttc   883
Val Gly Gln Val Ile Leu Leu Glu Leu Ala Ile Phe Ala Leu Ser Phe
                250                 255                 260

ttg ggc agc gca gtg atc atc ggt atg ttg gtg acc act ccg ctt aca   931
Leu Gly Ser Ala Val Ile Ile Gly Met Leu Val Thr Thr Pro Leu Thr
            265                 270                 275

ttc ctg ctg tat gcc tac gca ttc cag acc gcc agc ggt ggt ccc atc   979
Phe Leu Leu Tyr Ala Tyr Ala Phe Gln Thr Ala Ser Gly Gly Pro Ile
        280                 285                 290

atg cag cgt cag tagcagttag ttttacttag tca                        1014
Met Gln Arg Gln
    295
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<210> 2884
<211> 297
<212> PRT
<213> Corynebacterium glutamicum

<400> 2884

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Met Thr Ser Pro Tyr Gly Ser Gln Tyr Pro Gly Asp Asp Asn Asn Asn
  1               5                  10                  15

Trp Asn Ser Gln Phe Gly Asn Pro Ser Gly Glu Gln Asn Tyr Gly Gln
             20                  25                  30

Pro Tyr Gly Ala Pro Tyr Gly Gln Pro Tyr Gly Gln Pro Phe Asp Gln
         35                  40                  45

Gly Phe Asn Ala Tyr Ser Ser Pro Ile Pro Pro Glu Val Pro Gln Pro
     50                  55                  60

Ser Met Gln Glu Ala Gln Trp Arg Ser Phe Asp Leu Gly Thr Val Phe
 65                  70                  75                  80

Gly Gln Ala Trp Lys Gly Phe Thr Ala Thr Trp Gln Ala Trp Val Leu
                 85                  90                  95

Ser Ala Leu Ile Tyr Phe Ala Val Leu Leu Val Leu Met Phe Ala Trp
            100                 105                 110

Ile Leu Pro Met Val Ser Val Leu Ala Ala Thr Ser Ser Gly Ser Asp
        115                 120                 125

Ser Ala Ala Ile Ala Ala Thr Gly Gly Thr Ser Phe Phe Gly Phe Met
    130                 135                 140

Leu Met Ile Val Leu Ala Phe Ile Ser Phe Val Tyr Ser Leu Asn Cys
145                 150                 155                 160

Tyr Arg Asn Ala Ala Arg Val Val Arg Gly Glu Gln Ile Thr Ile Gln
                165                 170                 175

Ser Phe Phe Lys Met Lys Gly Leu Gly Lys Ala Leu Gly Ile Tyr Ile
            180                 185                 190

Leu Ile Asn Ile Val Ile Phe Ile Gly Met Ile Leu Leu Leu Ile Pro
        195                 200                 205

Gly Ile Ile Ala Ala Val Val Leu Ile Phe Ala Val Pro Val Ala Phe
    210                 215                 220

Gln Leu Arg Asp Ala Ser Ile Gly Asp Ala Phe Ser Ala Ser Trp Lys
225                 230                 235                 240

Ala Val Ser Lys Asn Val Gly Gln Val Ile Leu Leu Glu Leu Ala Ile
                245                 250                 255

Phe Ala Leu Ser Phe Leu Gly Ser Ala Val Ile Ile Gly Met Leu Val
            260                 265                 270

Thr Thr Pro Leu Thr Phe Leu Leu Tyr Ala Tyr Ala Phe Gln Thr Ala
        275                 280                 285
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```
Ser Gly Gly Pro Ile Met Gln Arg Gln
    290                 295


<210> 2885
<211> 669
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(646)
<223> RXA02757

<400> 2885
ttcggatcct tcgaccgttc aggcaatgca gatcgcgttg cacattccga aacagaatcc 60

gccccggcgg acagatgtgt tggaagcggc ggcgaggagt gtg gtc aag ctt tgc   115
                                            Val Val Lys Leu Cys
                                              1               5

ctc gac gaa cga gta tcc acc gat cct gat ttt cgg gcg gcc ttg gaa   163
Leu Asp Glu Arg Val Ser Thr Asp Pro Asp Phe Arg Ala Ala Leu Glu
                10                  15                  20

cgt tgg tac gga cac ttg att cgg aag gtg tca cgt cgc gct cgt aat   211
Arg Trp Tyr Gly His Leu Ile Arg Lys Val Ser Arg Arg Ala Arg Asn
            25                  30                  35

gcg gcg tgg gat cgg gtg caa gat tta ccc ggc gtg act gtg gaa gat   259
Ala Ala Trp Asp Arg Val Gln Asp Leu Pro Gly Val Thr Val Glu Asp
        40                  45                  50

gat gct gca aag gtt cgg gca ttt ttg ccc agc gca gtg gtg gat gtg   307
Asp Ala Ala Lys Val Arg Ala Phe Leu Pro Ser Ala Val Val Asp Val
    55                  60                  65

cct gca gat atc aaa aag ctg cag att tcc ggt acg gaa ttg cct ctc   355
Pro Ala Asp Ile Lys Lys Leu Gln Ile Ser Gly Thr Glu Leu Pro Leu
70                  75                  80                  85

gat gag ccg aat ccg atc aac gat gaa tac ccc gtt atc tac att gat   403
Asp Glu Pro Asn Pro Ile Asn Asp Glu Tyr Pro Val Ile Tyr Ile Asp
                90                  95                  100

gaa tcg ttg aag atg acg ctg gga aag gcc gct gcg cag gta gga cac   451
Glu Ser Leu Lys Met Thr Leu Gly Lys Ala Ala Ala Gln Val Gly His
            105                 110                 115

gca tcc atg ttg ctt gcc gcg cac caa ccg ttt gag tgg gtg gag cag   499
Ala Ser Met Leu Leu Ala Ala His Gln Pro Phe Glu Trp Val Glu Gln
        120                 125                 130

tgg gaa gca gcg gat ttt gcg ctg cac gtc agg gag att ccc tcg gag   547
Trp Glu Ala Ala Asp Phe Ala Leu His Val Arg Glu Ile Pro Ser Glu
    135                 140                 145

gag ttc ctg cgc ctt atc gag tct cct ggt gct gtt cca gtt cgc gat   595
Glu Phe Leu Arg Leu Ile Glu Ser Pro Gly Ala Val Pro Val Arg Asp
150                 155                 160                 165
```

```
ggc ggc ttt act gag gtt gcc ccc aac acc gtg acg gtt gtt gca att   643
Gly Gly Phe Thr Glu Val Ala Pro Asn Thr Val Thr Val Val Ala Ile
                170                 175                 180

cca taactaaacg agctttgatt aac                                   669
Pro
```

<210> 2886
<211> 182
<212> PRT
<213> Corynebacterium glutamicum

<400> 2886

```
Val Val Lys Leu Cys Leu Asp Glu Arg Val Ser Thr Asp Pro Asp Phe
  1               5                  10                  15

Arg Ala Ala Leu Glu Arg Trp Tyr Gly His Leu Ile Arg Lys Val Ser
             20                  25                  30

Arg Arg Ala Arg Asn Ala Ala Trp Asp Arg Val Gln Asp Leu Pro Gly
         35                  40                  45

Val Thr Val Glu Asp Asp Ala Ala Lys Val Arg Ala Phe Leu Pro Ser
     50                  55                  60

Ala Val Val Asp Val Pro Ala Asp Ile Lys Lys Leu Gln Ile Ser Gly
 65                  70                  75                  80

Thr Glu Leu Pro Leu Asp Glu Pro Asn Pro Ile Asn Asp Glu Tyr Pro
                 85                  90                  95

Val Ile Tyr Ile Asp Glu Ser Leu Lys Met Thr Leu Gly Lys Ala Ala
            100                 105                 110

Ala Gln Val Gly His Ala Ser Met Leu Leu Ala Ala His Gln Pro Phe
        115                 120                 125

Glu Trp Val Glu Gln Trp Glu Ala Ala Asp Phe Ala Leu His Val Arg
    130                 135                 140

Glu Ile Pro Ser Glu Glu Phe Leu Arg Leu Ile Glu Ser Pro Gly Ala
145                 150                 155                 160

Val Pro Val Arg Asp Gly Gly Phe Thr Glu Val Ala Pro Asn Thr Val
                165                 170                 175

Thr Val Val Ala Ile Pro
            180
```

<210> 2887
<211> 882
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(859)

<223> RXA02765

<400> 2887

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tctgaacttt tccgcatcga cccagatgag gtttaccccg acgacgacgc cacctgcgaa 60

ttcaacccat ggccgtatcc tcgcggattt taggagataa atg tct aat caa tta   115
                                            Met Ser Asn Gln Leu
                                              1               5

ccc gat cac gtc cgc gac gcc ttc caa gta ggt gcg gga cct gcc gaa   163
Pro Asp His Val Arg Asp Ala Phe Gln Val Gly Ala Gly Pro Ala Glu
                 10                  15                  20

caa ctc ggt caa gct tgg gac ttc gga ttc cgc gtc ggc aac act gtg   211
Gln Leu Gly Gln Ala Trp Asp Phe Gly Phe Arg Val Gly Asn Thr Val
             25                  30                  35

ttc gcc aaa gtg acg gcg ccg gaa gtg tcg ggc tgg tcg tcg aaa acc   259
Phe Ala Lys Val Thr Ala Pro Glu Val Ser Gly Trp Ser Ser Lys Thr
         40                  45                  50

cgc gaa acc ctg aaa cca gaa ggc gtg cgc gtc gta cga ccg atc cgc   307
Arg Glu Thr Leu Lys Pro Glu Gly Val Arg Val Val Arg Pro Ile Arg
     55                  60                  65

tcc acc gac ggc cga ttt gtg gtt gcg ggg tgg cgc gca tcg gtg ttc   355
Ser Thr Asp Gly Arg Phe Val Val Ala Gly Trp Arg Ala Ser Val Phe
 70                  75                  80                  85

tct acg gga acg atc agc aag cga gtc gat gag acg gtc gtt gcg ggt   403
Ser Thr Gly Thr Ile Ser Lys Arg Val Asp Glu Thr Val Val Ala Gly
                 90                  95                 100

ctt cgt ttg gca gat gca tta gtg gat acg cat gca ccg gaa cct gtg   451
Leu Arg Leu Ala Asp Ala Leu Val Asp Thr His Ala Pro Glu Pro Val
             105                 110                 115

gac aat gtg ttt aac cgt gct gat gtg cag gcc tgg gaa gag cag ccc   499
Asp Asn Val Phe Asn Arg Ala Asp Val Gln Ala Trp Glu Glu Gln Pro
         120                 125                 130

ggt cga atc ggt gaa ttg ttg gag ccg att aat cgc gtg aac cag gtt   547
Gly Arg Ile Gly Glu Leu Leu Glu Pro Ile Asn Arg Val Asn Gln Val
     135                 140                 145

ggt cat gcg gat atg ttg gcg aca acg ctg tat gcg gga act cag cca   595
Gly His Ala Asp Met Leu Ala Thr Thr Leu Tyr Ala Gly Thr Gln Pro
150                 155                 160                 165

cct gca gtg acg gat ttg gtg cca gtg ctg cgt ccg cat ggt ttc act   643
Pro Ala Val Thr Asp Leu Val Pro Val Leu Arg Pro His Gly Phe Thr
                170                 175                 180

gcg gca ttg gtg atc gtt gat ggg ttg ctg ctg ggt gcg gtt gat gag   691
Ala Ala Leu Val Ile Val Asp Gly Leu Leu Leu Gly Ala Val Asp Glu
            185                 190                 195

gga att ctg cgg agg ttt tcg cat ttg ccg gaa att gag cag ctg gtt   739
Gly Ile Leu Arg Arg Phe Ser His Leu Pro Glu Ile Glu Gln Leu Val
        200                 205                 210
```

```
ttg agg gca ttt ttg ttc cgt cga aac ttg cag gag ttc tct gag aac   787
Leu Arg Ala Phe Leu Phe Arg Arg Asn Leu Gln Glu Phe Ser Glu Asn
    215                 220                 225

aac gat ccg aat gtt att tcg aac cta aac agg gtg gaa tcg aca ctc   835
Asn Asp Pro Asn Val Ile Ser Asn Leu Asn Arg Val Glu Ser Thr Leu
230                 235                 240                 245

gtg tcg tat gtt tct gac aag att tgaggtatgt cggaatacaa acc         882
Val Ser Tyr Val Ser Asp Lys Ile
                250
```

<210> 2888
<211> 253
<212> PRT
<213> Corynebacterium glutamicum

<400> 2888

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Met Ser Asn Gln Leu Pro Asp His Val Arg Asp Ala Phe Gln Val Gly
  1               5                  10                  15

Ala Gly Pro Ala Glu Gln Leu Gly Gln Ala Trp Asp Phe Gly Phe Arg
             20                  25                  30

Val Gly Asn Thr Val Phe Ala Lys Val Thr Ala Pro Glu Val Ser Gly
         35                  40                  45

Trp Ser Ser Lys Thr Arg Glu Thr Leu Lys Pro Glu Gly Val Arg Val
     50                  55                  60

Val Arg Pro Ile Arg Ser Thr Asp Gly Arg Phe Val Val Ala Gly Trp
 65                  70                  75                  80

Arg Ala Ser Val Phe Ser Thr Gly Thr Ile Ser Lys Arg Val Asp Glu
                 85                  90                  95

Thr Val Val Ala Gly Leu Arg Leu Ala Asp Ala Leu Val Asp Thr His
            100                 105                 110

Ala Pro Glu Pro Val Asp Asn Val Phe Asn Arg Ala Asp Val Gln Ala
        115                 120                 125

Trp Glu Glu Gln Pro Gly Arg Ile Gly Glu Leu Leu Glu Pro Ile Asn
    130                 135                 140

Arg Val Asn Gln Val Gly His Ala Asp Met Leu Ala Thr Thr Leu Tyr
145                 150                 155                 160

Ala Gly Thr Gln Pro Pro Ala Val Thr Asp Leu Val Pro Val Leu Arg
                165                 170                 175

Pro His Gly Phe Thr Ala Ala Leu Val Ile Val Asp Gly Leu Leu Leu
            180                 185                 190

Gly Ala Val Asp Glu Gly Ile Leu Arg Arg Phe Ser His Leu Pro Glu
        195                 200                 205

Ile Glu Gln Leu Val Leu Arg Ala Phe Leu Phe Arg Arg Asn Leu Gln
    210                 215                 220
```

```
Glu Phe Ser Glu Asn Asn Asp Pro Asn Val Ile Ser Asn Leu Asn Arg
225                 230                 235                 240

Val Glu Ser Thr Leu Val Ser Tyr Val Ser Asp Lys Ile
                245                 250


<210> 2889
<211> 516
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(493)
<223> RXA02766

<400> 2889
atttctcgcc gcgccgcacg gtgacgccgg ccatgttgag tgctagttcg cgcatgggta 60

acaccttact ggcgtaaggc cagggcttag actggtaccc atg aca acc tca gaa   115
                                            Met Thr Thr Ser Glu
                                              1               5

aat ttt tat gat tct gtg ggc ggc gag gaa acg ttt tcc ctc atc gtc   163
Asn Phe Tyr Asp Ser Val Gly Gly Glu Glu Thr Phe Ser Leu Ile Val
                10                  15                  20

cac cgt ttt tat gaa cag gtc ccc aac gac gat att tta ggc ccg atg   211
His Arg Phe Tyr Glu Gln Val Pro Asn Asp Asp Ile Leu Gly Pro Met
            25                  30                  35

tat ccg ccg gat gat ttt gag ggc gcc gag cag cgt cta aag atg ttc   259
Tyr Pro Pro Asp Asp Phe Glu Gly Ala Glu Gln Arg Leu Lys Met Phe
        40                  45                  50

ctc agc cag tac tgg ggc ggc ccg aag gat tat cag gag cag cgt gga   307
Leu Ser Gln Tyr Trp Gly Gly Pro Lys Asp Tyr Gln Glu Gln Arg Gly
    55                  60                  65

cac cct cgt ctg cgc atg cgt cac gtc aat tac ccc atc ggc gtc acc   355
His Pro Arg Leu Arg Met Arg His Val Asn Tyr Pro Ile Gly Val Thr
70                  75                  80                  85

gca gcg gag cgt tgg ctg cag ctc atg tcc aat gca ctc gac ggc gtg   403
Ala Ala Glu Arg Trp Leu Gln Leu Met Ser Asn Ala Leu Asp Gly Val
                90                  95                  100

gat ttg acc gcg gag cag cgt gaa gcg att tgg gag cat atg gtg cgc   451
Asp Leu Thr Ala Glu Gln Arg Glu Ala Ile Trp Glu His Met Val Arg
            105                 110                 115

gcg gcc gat atg ctg atc aat tcc aac ccc gat ccg cac gct           493
Ala Ala Asp Met Leu Ile Asn Ser Asn Pro Asp Pro His Ala
        120                 125                 130

taacttctgc caaaaagtcg ttt                                        516


<210> 2890
<211> 131
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<212> PRT
<213> Corynebacterium glutamicum

<400> 2890
Met Thr Thr Ser Glu Asn Phe Tyr Asp Ser Val Gly Gly Glu Glu Thr
1 5 10 15

Phe Ser Leu Ile Val His Arg Phe Tyr Glu Gln Val Pro Asn Asp Asp
20 25 30

Ile Leu Gly Pro Met Tyr Pro Pro Asp Asp Phe Glu Gly Ala Glu Gln
35 40 45

Arg Leu Lys Met Phe Leu Ser Gln Tyr Trp Gly Gly Pro Lys Asp Tyr
50 55 60

Gln Glu Gln Arg Gly His Pro Arg Leu Arg Met Arg His Val Asn Tyr
65 70 75 80

Pro Ile Gly Val Thr Ala Ala Glu Arg Trp Leu Gln Leu Met Ser Asn
85 90 95

Ala Leu Asp Gly Val Asp Leu Thr Ala Glu Gln Arg Glu Ala Ile Trp
100 105 110

Glu His Met Val Arg Ala Ala Asp Met Leu Ile Asn Ser Asn Pro Asp
115 120 125

Pro His Ala
130

<210> 2891
<211> 494
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(471)
<223> RXA02774

<400> 2891
ccc tgc cca cca aca cag aag ctg ctc tat gca cag atg cgt gaa att 48
Pro Cys Pro Pro Thr Gln Lys Leu Leu Tyr Ala Gln Met Arg Glu Ile
1 5 10 15

gca gcc gaa ctt aca gcc tgt gac gct act cgc gga ctc cat gcc gaa 96
Ala Ala Glu Leu Thr Ala Cys Asp Ala Thr Arg Gly Leu His Ala Glu
20 25 30

gtg gct gcc gaa tgg ctt agt gac gcc ata acc ggc gaa ccc acc tct 144
Val Ala Ala Glu Trp Leu Ser Asp Ala Ile Thr Gly Glu Pro Thr Ser
35 40 45

atc gag att gac ccc cac cgc aac ctg ttc tac gca ctt aat gtt gag 192
Ile Glu Ile Asp Pro His Arg Asn Leu Phe Tyr Ala Leu Asn Val Glu
50 55 60

cac ccg cga ctc cat gaa ctc ttt gcc ggt tac gct aca cgc ctt gat 240
His Pro Arg Leu His Glu Leu Phe Ala Gly Tyr Ala Thr Arg Leu Asp

```
 65                  70                  75                  80

gaa ctc gac cgc gca ccg cag cag tgt gag tcg cgt caa tat ttt ctt   288
Glu Leu Asp Arg Ala Pro Gln Gln Cys Glu Ser Arg Gln Tyr Phe Leu
                85                  90                  95

gat tat gtc tgt gct gac aac cct ttt ggc tca gac aaa cca gag ggc   336
Asp Tyr Val Cys Ala Asp Asn Pro Phe Gly Ser Asp Lys Pro Glu Gly
            100                 105                 110

att atc gtg ctg ctc gct gat cac gtg ctg gca gca gat cca gtg aca   384
Ile Ile Val Leu Leu Ala Asp His Val Leu Ala Ala Asp Pro Val Thr
        115                 120                 125

aac aag ccg gca ctc aaa tca gag gca ttc cct act gtc aca gac tat   432
Asn Lys Pro Ala Leu Lys Ser Glu Ala Phe Pro Thr Val Thr Asp Tyr
    130                 135                 140

tgc cgc act cac tct gct aaa cca aca gac att ctc att taaggatttt    481
Cys Arg Thr His Ser Ala Lys Pro Thr Asp Ile Leu Ile
145                 150                 155

agtcaccatg acg                                                   494


<210> 2892
<211> 157
<212> PRT
<213> Corynebacterium glutamicum

<400> 2892
Pro Cys Pro Pro Thr Gln Lys Leu Leu Tyr Ala Gln Met Arg Glu Ile
  1               5                  10                  15

Ala Ala Glu Leu Thr Ala Cys Asp Ala Thr Arg Gly Leu His Ala Glu
             20                  25                  30

Val Ala Ala Glu Trp Leu Ser Asp Ala Ile Thr Gly Glu Pro Thr Ser
         35                  40                  45

Ile Glu Ile Asp Pro His Arg Asn Leu Phe Tyr Ala Leu Asn Val Glu
     50                  55                  60

His Pro Arg Leu His Glu Leu Phe Ala Gly Tyr Ala Thr Arg Leu Asp
 65                  70                  75                  80

Glu Leu Asp Arg Ala Pro Gln Gln Cys Glu Ser Arg Gln Tyr Phe Leu
                85                  90                  95

Asp Tyr Val Cys Ala Asp Asn Pro Phe Gly Ser Asp Lys Pro Glu Gly
            100                 105                 110

Ile Ile Val Leu Leu Ala Asp His Val Leu Ala Ala Asp Pro Val Thr
        115                 120                 125

Asn Lys Pro Ala Leu Lys Ser Glu Ala Phe Pro Thr Val Thr Asp Tyr
    130                 135                 140

Cys Arg Thr His Ser Ala Lys Pro Thr Asp Ile Leu Ile
145                 150                 155
```

<210> 2893
<211> 348
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(325)
<223> RXA02775

<400> 2893
gcccccacca tctttggcac tgagattgtg ttcgattaac taccactgct gcacacacac 60

atacaacacc tctcacacac aaacaagaaa gggtcacccc atg acc acc gtt caa 115
Met Thr Thr Val Gln
1 5

gta tcc acc cgc act gtg cgc gaa cac cgt ttt act gtg cca gtg gac 163
Val Ser Thr Arg Thr Val Arg Glu His Arg Phe Thr Val Pro Val Asp
10 15 20

tac gct gtc ggc gcc acc att tca gaa atc tat gct gcc tgt gcc atg 211
Tyr Ala Val Gly Ala Thr Ile Ser Glu Ile Tyr Ala Ala Cys Ala Met
25 30 35

gcc gaa aag aaa gcc aac aac ctt ggg ctt aac act act aag gac gat 259
Ala Glu Lys Lys Ala Asn Asn Leu Gly Leu Asn Thr Thr Lys Asp Asp
40 45 50

tgg gca cga gtc act gtc act gat aat gct gtt gtg ttc att gtc gag 307
Trp Ala Arg Val Thr Val Thr Asp Asn Ala Val Val Phe Ile Val Glu
55 60 65

aat gtt atc ggg aat act tagaattgtg tgctccttaa cgg 348
Asn Val Ile Gly Asn Thr
70 75

<210> 2894
<211> 75
<212> PRT
<213> Corynebacterium glutamicum

<400> 2894
Met Thr Thr Val Gln Val Ser Thr Arg Thr Val Arg Glu His Arg Phe
1 5 10 15

Thr Val Pro Val Asp Tyr Ala Val Gly Ala Thr Ile Ser Glu Ile Tyr
20 25 30

Ala Ala Cys Ala Met Ala Glu Lys Lys Ala Asn Asn Leu Gly Leu Asn
35 40 45

Thr Thr Lys Asp Asp Trp Ala Arg Val Thr Val Thr Asp Asn Ala Val
50 55 60

Val Phe Ile Val Glu Asn Val Ile Gly Asn Thr
65 70 75

<210> 2895
<211> 465
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(442)
<223> RXA02776

<400> 2895
gcagcaccta gcaatgcagc cgaggcagcc ccttcaggtt ttgagccagg tacggctatt 60

caagttgtat aatccttcat tcgatgatca aacaccttcg gtg ctc tat cct gtt 115
Val Leu Tyr Pro Val
1 5

gaa gca gga acg gtg tct ctc gtt gat gta aag aaa gcg gct agc cgt 163
Glu Ala Gly Thr Val Ser Leu Val Asp Val Lys Lys Ala Ala Ser Arg
10 15 20

gcc ttt gaa cag tgg gaa aag cac aac gag tcc gct ggt gat gtc ggt 211
Ala Phe Glu Gln Trp Glu Lys His Asn Glu Ser Ala Gly Asp Val Gly
25 30 35

gat gat ctt tca ctg cag agt atc gta gat ctc att gag cgt gac act 259
Asp Asp Leu Ser Leu Gln Ser Ile Val Asp Leu Ile Glu Arg Asp Thr
40 45 50

ttc ccc acc gac gat gag caa gag ctc aat aat gtg gct ttg ctt atc 307
Phe Pro Thr Asp Asp Glu Gln Glu Leu Asn Asn Val Ala Leu Leu Ile
55 60 65

ggc gaa ctc ctg gtg agg gag gcc ggt gga gag tgg acg tcg tac atc 355
Gly Glu Leu Leu Val Arg Glu Ala Gly Gly Glu Trp Thr Ser Tyr Ile
70 75 80 85

tca aag aaa aat gat gaa gat gaa tcg ctg gag att ttc ggg gtt ttt 403
Ser Lys Lys Asn Asp Glu Asp Glu Ser Leu Glu Ile Phe Gly Val Phe
90 95 100

ggc acc ggt ggc act gaa gga tta tct gta gtg ggt aat tgagttcgca 452
Gly Thr Gly Gly Thr Glu Gly Leu Ser Val Val Gly Asn
105 110

tggttagtga aaa 465

<210> 2896
<211> 114
<212> PRT
<213> Corynebacterium glutamicum

<400> 2896
Val Leu Tyr Pro Val Glu Ala Gly Thr Val Ser Leu Val Asp Val Lys
1 5 10 15

Lys Ala Ala Ser Arg Ala Phe Glu Gln Trp Glu Lys His Asn Glu Ser
20 25 30

Ala Gly Asp Val Gly Asp Asp Leu Ser Leu Gln Ser Ile Val Asp Leu

```
         35                  40                  45

Ile Glu Arg Asp Thr Phe Pro Thr Asp Asp Glu Gln Glu Leu Asn Asn
     50                  55                  60

Val Ala Leu Leu Ile Gly Glu Leu Leu Val Arg Glu Ala Gly Gly Glu
 65                  70                  75                  80

Trp Thr Ser Tyr Ile Ser Lys Lys Asn Asp Glu Asp Glu Ser Leu Glu
                 85                  90                  95

Ile Phe Gly Val Phe Gly Thr Gly Gly Thr Glu Gly Leu Ser Val Val
            100                 105                 110

Gly Asn
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<210> 2897
<211> 1230
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1207)
<223> RXA02777

<400> 2897

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ggtcgcacca caccaactac tgtttcttct gtaatttgca ctgaaactat cgcctacact 60

gtcactgcta ccatcacaat cggttgctag taggctacaa atg aac cgc ccc ctt   115
                                          Met Asn Arg Pro Leu
                                            1               5

caa agt caa aat ttt tca ata acc agc gaa tgg gca aat gcc acg ttc   163
Gln Ser Gln Asn Phe Ser Ile Thr Ser Glu Trp Ala Asn Ala Thr Phe
                10                  15                  20

aac gat atc gaa gac tct ttg gag ggg tct ttt gac atc gaa cca ggc   211
Asn Asp Ile Glu Asp Ser Leu Glu Gly Ser Phe Asp Ile Glu Pro Gly
            25                  30                  35

caa tac att gga cgc gga gaa tac ttc gta gct act tct gga acg ggt   259
Gln Tyr Ile Gly Arg Gly Glu Tyr Phe Val Ala Thr Ser Gly Thr Gly
        40                  45                  50

tcc aaa aag ttt atc aag gtg gtt ttg ggt gac ggt atc gat agc gaa   307
Ser Lys Lys Phe Ile Lys Val Val Leu Gly Asp Gly Ile Asp Ser Glu
    55                  60                  65

cta aat cgt cgc atc gaa ggt gaa att ctt gca agt agt ctc cat ctt   355
Leu Asn Arg Arg Ile Glu Gly Glu Ile Leu Ala Ser Ser Leu His Leu
70                  75                  80                  85

cca tcc aca gac cta atc tct cct gtc gta att cag tat gtg aaa gag   403
Pro Ser Thr Asp Leu Ile Ser Pro Val Val Ile Gln Tyr Val Lys Glu
                90                  95                 100

tct tct aat ttt ccc ggt gac ttc tac atc gtg tcc gac ttc aaa gac   451
Ser Ser Asn Phe Pro Gly Asp Phe Tyr Ile Val Ser Asp Phe Lys Asp
```

```
            105                 110                 115

gac aca gaa act tta gag cta tct aag gct tct cta ccc ctc act gac   499
Asp Thr Glu Thr Leu Glu Leu Ser Lys Ala Ser Leu Pro Leu Thr Asp
        120                 125                 130

tta gcc aag atc gga gcg ttt ctc ttt cgt ttg gaa tct gta aca gtt   547
Leu Ala Lys Ile Gly Ala Phe Leu Phe Arg Leu Glu Ser Val Thr Val
    135                 140                 145

ccc cct caa aat cct gca agg cga gca atg gat gtt ttg gat gga ctt   595
Pro Pro Gln Asn Pro Ala Arg Arg Ala Met Asp Val Leu Asp Gly Leu
150                 155                 160                 165

tct ctt ctt gca aat aaa ggc aac att gaa aca ggc gca caa tta aca   643
Ser Leu Leu Ala Asn Lys Gly Asn Ile Glu Thr Gly Ala Gln Leu Thr
                170                 175                 180

aaa gga act ata caa gct ctt gaa atc att aat caa gaa gcg acc aac   691
Lys Gly Thr Ile Gln Ala Leu Glu Ile Ile Asn Gln Glu Ala Thr Asn
            185                 190                 195

atc gag aat gca ctt gaa aaa gta act aaa gta gga tca cgg aag ttt   739
Ile Glu Asn Ala Leu Glu Lys Val Thr Lys Val Gly Ser Arg Lys Phe
        200                 205                 210

ttc tcg cat gga gat ctt aaa ttt tct cag ttc tta att aat ggt gaa   787
Phe Ser His Gly Asp Leu Lys Phe Ser Gln Phe Leu Ile Asn Gly Glu
    215                 220                 225

acc gga aag att ttc cta tgt gac tgg gaa gaa tgc ggt agt gca cat   835
Thr Gly Lys Ile Phe Leu Cys Asp Trp Glu Glu Cys Gly Ser Ala His
230                 235                 240                 245

ttc gca aat gac cta tgt ttt ctc gca ggt gat ttg ttc tat agc aca   883
Phe Ala Asn Asp Leu Cys Phe Leu Ala Gly Asp Leu Phe Tyr Ser Thr
                250                 255                 260

att cgg gaa ctg gtg gat acc aac atc aaa aac att aaa ggc tcc tcg   931
Ile Arg Glu Leu Val Asp Thr Asn Ile Lys Asn Ile Lys Gly Ser Ser
            265                 270                 275

atc att cag gaa gcc tac gat aat gca acg ctt gag gct gta tca aaa   979
Ile Ile Gln Glu Ala Tyr Asp Asn Ala Thr Leu Glu Ala Val Ser Lys
        280                 285                 290

gta aat gca ata tta act ggc tat tcc tca gag agg ggt tac tct ctc   1027
Val Asn Ala Ile Leu Thr Gly Tyr Ser Ser Glu Arg Gly Tyr Ser Leu
    295                 300                 305

acc tcg gac gaa aaa cga atc att agt atc aga atc gga ttg gct ggt   1075
Thr Ser Asp Glu Lys Arg Ile Ile Ser Ile Arg Ile Gly Leu Ala Gly
310                 315                 320                 325

cta ttt cga ctt tac act gtg agc gct aaa tct aat gag tta cgc ccg   1123
Leu Phe Arg Leu Tyr Thr Val Ser Ala Lys Ser Asn Glu Leu Arg Pro
                330                 335                 340

cgc gaa tta gcc tta gcc tcc atc gga atg caa att act tta ggt caa   1171
Arg Glu Leu Ala Leu Ala Ser Ile Gly Met Gln Ile Thr Leu Gly Gln
            345                 350                 355
```

```
gca ccc aat ctg gtg ttt aca gat agc aag gtg gtt taagtgagga        1217
Ala Pro Asn Leu Val Phe Thr Asp Ser Lys Val Val
        360                 365

atttgcacga aac                                                   1230
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<210> 2898
<211> 369
<212> PRT
<213> Corynebacterium glutamicum

<400> 2898

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Met Asn Arg Pro Leu Gln Ser Gln Asn Phe Ser Ile Thr Ser Glu Trp
  1               5                  10                  15

Ala Asn Ala Thr Phe Asn Asp Ile Glu Asp Ser Leu Glu Gly Ser Phe
             20                  25                  30

Asp Ile Glu Pro Gly Gln Tyr Ile Gly Arg Gly Glu Tyr Phe Val Ala
         35                  40                  45

Thr Ser Gly Thr Gly Ser Lys Lys Phe Ile Lys Val Val Leu Gly Asp
     50                  55                  60

Gly Ile Asp Ser Glu Leu Asn Arg Arg Ile Glu Gly Glu Ile Leu Ala
 65                  70                  75                  80

Ser Ser Leu His Leu Pro Ser Thr Asp Leu Ile Ser Pro Val Val Ile
                 85                  90                  95

Gln Tyr Val Lys Glu Ser Ser Asn Phe Pro Gly Asp Phe Tyr Ile Val
            100                 105                 110

Ser Asp Phe Lys Asp Asp Thr Glu Thr Leu Glu Leu Ser Lys Ala Ser
        115                 120                 125

Leu Pro Leu Thr Asp Leu Ala Lys Ile Gly Ala Phe Leu Phe Arg Leu
    130                 135                 140

Glu Ser Val Thr Val Pro Pro Gln Asn Pro Ala Arg Arg Ala Met Asp
145                 150                 155                 160

Val Leu Asp Gly Leu Ser Leu Leu Ala Asn Lys Gly Asn Ile Glu Thr
                165                 170                 175

Gly Ala Gln Leu Thr Lys Gly Thr Ile Gln Ala Leu Glu Ile Ile Asn
            180                 185                 190

Gln Glu Ala Thr Asn Ile Glu Asn Ala Leu Glu Lys Val Thr Lys Val
        195                 200                 205

Gly Ser Arg Lys Phe Phe Ser His Gly Asp Leu Lys Phe Ser Gln Phe
    210                 215                 220

Leu Ile Asn Gly Glu Thr Gly Lys Ile Phe Leu Cys Asp Trp Glu Glu
225                 230                 235                 240

Cys Gly Ser Ala His Phe Ala Asn Asp Leu Cys Phe Leu Ala Gly Asp
                245                 250                 255
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Leu Phe Tyr Ser Thr Ile Arg Glu Leu Val Asp Thr Asn Ile Lys Asn
            260                 265                 270

Ile Lys Gly Ser Ser Ile Ile Gln Glu Ala Tyr Asp Asn Ala Thr Leu
        275                 280                 285

Glu Ala Val Ser Lys Val Asn Ala Ile Leu Thr Gly Tyr Ser Ser Glu
    290                 295                 300

Arg Gly Tyr Ser Leu Thr Ser Asp Glu Lys Arg Ile Ile Ser Ile Arg
305                 310                 315                 320

Ile Gly Leu Ala Gly Leu Phe Arg Leu Tyr Thr Val Ser Ala Lys Ser
                325                 330                 335

Asn Glu Leu Arg Pro Arg Glu Leu Ala Leu Ala Ser Ile Gly Met Gln
            340                 345                 350

Ile Thr Leu Gly Gln Ala Pro Asn Leu Val Phe Thr Asp Ser Lys Val
        355                 360                 365

Val
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<210> 2899
<211> 348
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(325)
<223> RXA02778

<400> 2899

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ctccgatttc tgaggtcagt acgcgctcct gtctaacttc taccacccag cccaaccaat 60

cgtttttcaa gggttcaccg aagcaactgt tgagcacctc atg cag gtc att gag   115
                                            Met Gln Val Ile Glu
                                              1               5

acg ctt gat ccc gat cag cgc gca gcg gtg ctc gct gca gcg ata ccg   163
Thr Leu Asp Pro Asp Gln Arg Ala Ala Val Leu Ala Ala Ala Ile Pro
                 10                  15                  20

cgc gag gct aag atc ctg ggg cga aaa gta act ctt cgc cct ggt tgg   211
Arg Glu Ala Lys Ile Leu Gly Arg Lys Val Thr Leu Arg Pro Gly Trp
             25                  30                  35

ggc aat atg cgc gta cac gtc gtg att gca gtt atc ttt atc aag ttt   259
Gly Asn Met Arg Val His Val Val Ile Ala Val Ile Phe Ile Lys Phe
         40                  45                  50

ttg caa ccg gat ctt cgc cag gcg ctg cta aca aca ggt gat gcc gta   307
Leu Gln Pro Asp Leu Arg Gln Ala Leu Leu Thr Thr Gly Asp Ala Val
     55                  60                  65

ctt gtc gaa gat gat acc tgaggcgcct tctggggcgt cga                 348
Leu Val Glu Asp Asp Thr
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70 75

<210> 2900
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<212> PRT
<213> Corynebacterium glutamicum

<400> 2900
Met Gln Val Ile Glu Thr Leu Asp Pro Asp Gln Arg Ala Ala Val Leu
1 5 10 15

Ala Ala Ala Ile Pro Arg Glu Ala Lys Ile Leu Gly Arg Lys Val Thr
20 25 30

Leu Arg Pro Gly Trp Gly Asn Met Arg Val His Val Val Ile Ala Val
35 40 45

Ile Phe Ile Lys Phe Leu Gln Pro Asp Leu Arg Gln Ala Leu Leu Thr
50 55 60

Thr Gly Asp Ala Val Leu Val Glu Asp Asp Thr
65 70 75

<210> 2901
<211> 402
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(379)
<223> RXA02779

<400> 2901
ctcaaaggag actgcacatc atgttcctca ccaaagatat gctcgcacgt tttcctgcaa 60

gtttgaattt gccaatgcac agtgctcaga accagaagaa atg ggc gaa tac ttc 115
Met Gly Glu Tyr Phe
1 5

cag gtc gtt caa aac atc gcc atg aca ctg ggt gct ggc gaa agc gtt 163
Gln Val Val Gln Asn Ile Ala Met Thr Leu Gly Ala Gly Glu Ser Val
10 15 20

gat ctt gtt gtc cgc gaa tac atc aac gat gtg gaa ggc aac ccg acc 211
Asp Leu Val Val Arg Glu Tyr Ile Asn Asp Val Glu Gly Asn Pro Thr
25 30 35

atc tat cac ggt atg ccg ctg cgt act gaa tac cgc gca ttc atc gac 259
Ile Tyr His Gly Met Pro Leu Arg Thr Glu Tyr Arg Ala Phe Ile Asp
40 45 50

ctt gat cac tgt gat ccg tcc gct ggt gag cct gag cct cgc tta ttg 307
Leu Asp His Cys Asp Pro Ser Ala Gly Glu Pro Glu Pro Arg Leu Leu
55 60 65

ggg gtt act ccc tac tgg cac ccc tcc gtg atg gag aaa gct ctt cgc 355
Gly Val Thr Pro Tyr Trp His Pro Ser Val Met Glu Lys Ala Leu Arg
70 75 80 85

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ctt tgc ttc aag cga tgt tgg tgc tgaattcggt cacatcaacg atg          402
Leu Cys Phe Lys Arg Cys Trp Cys
                 90


<210> 2902
<211> 93
<212> PRT
<213> Corynebacterium glutamicum

<400> 2902
Met Gly Glu Tyr Phe Gln Val Val Gln Asn Ile Ala Met Thr Leu Gly
  1               5                  10                  15

Ala Gly Glu Ser Val Asp Leu Val Val Arg Glu Tyr Ile Asn Asp Val
             20                  25                  30

Glu Gly Asn Pro Thr Ile Tyr His Gly Met Pro Leu Arg Thr Glu Tyr
         35                  40                  45

Arg Ala Phe Ile Asp Leu Asp His Cys Asp Pro Ser Ala Gly Glu Pro
     50                  55                  60

Glu Pro Arg Leu Leu Gly Val Thr Pro Tyr Trp His Pro Ser Val Met
 65                  70                  75                  80

Glu Lys Ala Leu Arg Leu Cys Phe Lys Arg Cys Trp Cys
                 85                  90


<210> 2903
<211> 450
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(427)
<223> RXA02780

<400> 2903
atggagaaag ctcttcgcct ttgcttcaag cgatgttggt gctgaattcg gtcacatcaa 60

cgatgattac cgcacctacc gtgcccacaa agacagcctc atg tcc aag ttc cat   115
                                            Met Ser Lys Phe His
                                              1               5

aca cac cgt gat gat gtc att tca cgt atc act gca cta cta ccc cag   163
Thr His Arg Asp Asp Val Ile Ser Arg Ile Thr Ala Leu Leu Pro Gln
                 10                  15                  20

ctt cgt gca caa gag ctg caa ggt caa tgg tct gtg gac atc atg aaa   211
Leu Arg Ala Gln Glu Leu Gln Gly Gln Trp Ser Val Asp Ile Met Lys
             25                  30                  35

aac ggg gag gat ttc tac ctc att gac atg gct ctc atg tgc gag tcc   259
Asn Gly Glu Asp Phe Tyr Leu Ile Asp Met Ala Leu Met Cys Glu Ser
         40                  45                  50

gca ctg tct gaa cta ctc act gtt aca gat gag tac gcc aca gtc gag   307
```

```
Ala Leu Ser Glu Leu Leu Thr Val Thr Asp Glu Tyr Ala Thr Val Glu
     55                  60                  65

ccg agt gtc atc aat gac ttc gcc aac cag ctg gtc att gat tat gac   355
Pro Ser Val Ile Asn Asp Phe Ala Asn Gln Leu Val Ile Asp Tyr Asp
 70                  75                  80                  85

gag cac gat atg ggc ttt gat cga gac ttt cca gca ggt gtg tat aac   403
Glu His Asp Met Gly Phe Asp Arg Asp Phe Pro Ala Gly Val Tyr Asn
                 90                  95                 100

acc cga caa gca agt gct atc aac taaaaaatac acacatccac acc         450
Thr Arg Gln Ala Ser Ala Ile Asn
            105


<210> 2904
<211> 109
<212> PRT
<213> Corynebacterium glutamicum

<400> 2904
Met Ser Lys Phe His Thr His Arg Asp Asp Val Ile Ser Arg Ile Thr
  1               5                  10                  15

Ala Leu Leu Pro Gln Leu Arg Ala Gln Glu Leu Gln Gly Gln Trp Ser
             20                  25                  30

Val Asp Ile Met Lys Asn Gly Glu Asp Phe Tyr Leu Ile Asp Met Ala
         35                  40                  45

Leu Met Cys Glu Ser Ala Leu Ser Glu Leu Leu Thr Val Thr Asp Glu
     50                  55                  60

Tyr Ala Thr Val Glu Pro Ser Val Ile Asn Asp Phe Ala Asn Gln Leu
 65                  70                  75                  80

Val Ile Asp Tyr Asp Glu His Asp Met Gly Phe Asp Arg Asp Phe Pro
                 85                  90                  95

Ala Gly Val Tyr Asn Thr Arg Gln Ala Ser Ala Ile Asn
            100                 105


<210> 2905
<211> 672
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(649)
<223> RXA02783

<400> 2905
acaagcttca tgcaacccat aacctcagtg ctgttttgcc taccgaaact actgactcac 60

gtgtggcaac caccgctttc gccgtacact cacactgtcg gtg gtc tct ggt tca   115
                                            Val Val Ser Gly Ser
                                              1               5
```

```
cgc gct gct gca ttc ttg aac agc aac cat att cag ggt gct gtc tcg   163
Arg Ala Ala Ala Phe Leu Asn Ser Asn His Ile Gln Gly Ala Val Ser
                10                  15                  20

gcc act aag cac ttt gcc ctg tgc gac aac aac gac gat att cga gca   211
Ala Thr Lys His Phe Ala Leu Cys Asp Asn Asn Asp Asp Ile Arg Ala
            25                  30                  35

ctc ctg tcg gtg cgc tca cca aaa aac aat gcc cgc atg tat cgc aaa   259
Leu Leu Ser Val Arg Ser Pro Lys Asn Asn Ala Arg Met Tyr Arg Lys
        40                  45                  50

aaa ggc aca tgg gaa atc cag cgc tat gcg aca ctc ggt aac gtc cct   307
Lys Gly Thr Trp Glu Ile Gln Arg Tyr Ala Thr Leu Gly Asn Val Pro
    55                  60                  65

ggc ggt ttt act agg ctg ctg aag ttt gcc gag cac aca ctc aac gaa   355
Gly Gly Phe Thr Arg Leu Leu Lys Phe Ala Glu His Thr Leu Asn Glu
70                  75                  80                  85

cac agc aca gta ctc aag caa tgg atc tca ttt tct gct gct gat gtc   403
His Ser Thr Val Leu Lys Gln Trp Ile Ser Phe Ser Ala Ala Asp Val
                90                  95                  100

tct gac ggc agc ctg tat cga act gcc ggt ttt acc gcc gag caa cag   451
Ser Asp Gly Ser Leu Tyr Arg Thr Ala Gly Phe Thr Ala Glu Gln Gln
            105                 110                 115

ctt gca ccg gat tat cgc tat gtc ggt ggc gca aca ggt tgg cgc cga   499
Leu Ala Pro Asp Tyr Arg Tyr Val Gly Gly Ala Thr Gly Trp Arg Arg
        120                 125                 130

aca ccc aaa gaa agc ttc cag cgc aaa cgc ttt aga gac gac cca gcg   547
Thr Pro Lys Glu Ser Phe Gln Arg Lys Arg Phe Arg Asp Asp Pro Ala
    135                 140                 145

ttg cta tgg aac gaa tct tgg aca gag cac gaa gca gcg ctc aac aac   595
Leu Leu Trp Asn Glu Ser Trp Thr Glu His Glu Ala Ala Leu Asn Asn
150                 155                 160                 165

gag ctc tac aga atc tac gat gcc ggc aaa acc cgg tgg gtt aaa aat   643
Glu Leu Tyr Arg Ile Tyr Asp Ala Gly Lys Thr Arg Trp Val Lys Asn
                170                 175                 180

gtt gct tgattctgca gattagttac tga                                672
Val Ala
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<210> 2906
<211> 183
<212> PRT
<213> Corynebacterium glutamicum

<400> 2906

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Val Val Ser Gly Ser Arg Ala Ala Ala Phe Leu Asn Ser Asn His Ile
  1               5                  10                  15

Gln Gly Ala Val Ser Ala Thr Lys His Phe Ala Leu Cys Asp Asn Asn
            20                  25                  30
```

```
Asp Asp Ile Arg Ala Leu Leu Ser Val Arg Ser Pro Lys Asn Asn Ala
         35                  40                  45

Arg Met Tyr Arg Lys Lys Gly Thr Trp Glu Ile Gln Arg Tyr Ala Thr
     50                  55                  60

Leu Gly Asn Val Pro Gly Gly Phe Thr Arg Leu Leu Lys Phe Ala Glu
 65                  70                  75                  80

His Thr Leu Asn Glu His Ser Thr Val Leu Lys Gln Trp Ile Ser Phe
                 85                  90                  95

Ser Ala Ala Asp Val Ser Asp Gly Ser Leu Tyr Arg Thr Ala Gly Phe
            100                 105                 110

Thr Ala Glu Gln Gln Leu Ala Pro Asp Tyr Arg Tyr Val Gly Gly Ala
        115                 120                 125

Thr Gly Trp Arg Arg Thr Pro Lys Glu Ser Phe Gln Arg Lys Arg Phe
    130                 135                 140

Arg Asp Asp Pro Ala Leu Leu Trp Asn Glu Ser Trp Thr Glu His Glu
145                 150                 155                 160

Ala Ala Leu Asn Asn Glu Leu Tyr Arg Ile Tyr Asp Ala Gly Lys Thr
                165                 170                 175

Arg Trp Val Lys Asn Val Ala
            180
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Sequence Listing.ST25.txt

<210> 2907
<211> 309
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(286)
<223> RXA02784

<400> 2907
agctgcaact caggtagaag aaacaacagt cgcccgagtt gaacacgata cttacgacac 60

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tattgctaac cagctacaag atgccggtgt ctatgacgat gtg gcc ttt gcc gaa   115
                                              Val Ala Phe Ala Glu
                                                1               5

ggc tac tac cag gaa atg gct gag gtt gta tgt gaa gca cgc gaa gag   163
Gly Tyr Tyr Gln Glu Met Ala Glu Val Val Cys Glu Ala Arg Glu Glu
                10                  15                  20

ggt atc acc cac gag gac acc ctg cat atg ctc aat gac atg atg gca   211
Gly Ile Thr His Glu Asp Thr Leu His Met Leu Asn Asp Met Met Ala
            25                  30                  35

atg aaa cga tct ggc gaa gta ctc aat acg ctc gct gat gtt ctc tat   259
Met Lys Arg Ser Gly Glu Val Leu Asn Thr Leu Ala Asp Val Leu Tyr
        40                  45                  50

gca aat gaa tgc cct gaa tat cga atc taaattgttg gtcactctgc         306
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Ala Asn Glu Cys Pro Glu Tyr Arg Ile
     55                  60

ata                                                                    309


<210> 2908
<211> 62
<212> PRT
<213> Corynebacterium glutamicum

<400> 2908
Val Ala Phe Ala Glu Gly Tyr Tyr Gln Glu Met Ala Glu Val Val Cys
  1               5                  10                  15

Glu Ala Arg Glu Glu Gly Ile Thr His Glu Asp Thr Leu His Met Leu
             20                  25                  30

Asn Asp Met Met Ala Met Lys Arg Ser Gly Glu Val Leu Asn Thr Leu
         35                  40                  45

Ala Asp Val Leu Tyr Ala Asn Glu Cys Pro Glu Tyr Arg Ile
     50                  55                  60


<210> 2909
<211> 830
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(807)
<223> RXA02786

<400> 2909
atc ctg cgc aac ctc ggc caa tcg ctg ggc agc ctg cac gcc gcc acc   48
Ile Leu Arg Asn Leu Gly Gln Ser Leu Gly Ser Leu His Ala Ala Thr
  1               5                  10                  15

gca gac cgc gaa gaa gac ttc aac att ctg ctc aac cgt atg ctg gcc   96
Ala Asp Arg Glu Glu Asp Phe Asn Ile Leu Leu Asn Arg Met Leu Ala
             20                  25                  30

aaa tac cca gcc aca gct gag atg cag aaa aac cgc gat agg ttg ctg   144
Lys Tyr Pro Ala Thr Ala Glu Met Gln Lys Asn Arg Asp Arg Leu Leu
         35                  40                  45

ccc gca gca att gag gtg ggt aaa aag ata ctt gtc gac gcc ggg gtc   192
Pro Ala Ala Ile Glu Val Gly Lys Lys Ile Leu Val Asp Ala Gly Val
     50                  55                  60

acc gtt cca gaa gtc gtc gag gag ttt gcc cgc gta gct cgg cga cgc   240
Thr Val Pro Glu Val Val Glu Glu Phe Ala Arg Val Ala Arg Arg Arg
 65                  70                  75                  80

ctg att tcc gga cgc cac cgt gcc ttc aca cct ttt gac ttg tca ccc   288
Leu Ile Ser Gly Arg His Arg Ala Phe Thr Pro Phe Asp Leu Ser Pro
                 85                  90                  95

gac aac atc atc gtg gct gaa cgc acc cac ttc ctg gac tac gaa gtt   336
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```
Asp Asn Ile Ile Val Ala Glu Arg Thr His Phe Leu Asp Tyr Glu Val
            100                 105                 110

gcc ggt ttc agg gat gcc acc ttt gat gtt gct tgt gtg atc gca ggt   384
Ala Gly Phe Arg Asp Ala Thr Phe Asp Val Ala Cys Val Ile Ala Gly
        115                 120                 125

ttc ccg caa ttc gtg ttc agc cgc ccc atc tct gat gat gag gta gac   432
Phe Pro Gln Phe Val Phe Ser Arg Pro Ile Ser Asp Asp Glu Val Asp
    130                 135                 140

gaa ctc att gaa tcc tgg gtc caa gaa gtc cgt gga atc tgg ccc aat   480
Glu Leu Ile Glu Ser Trp Val Gln Glu Val Arg Gly Ile Trp Pro Asn
145                 150                 155                 160

gtg aac aat gaa gag cgc ctc caa gca cgt atc gtg acc gct ctc atc   528
Val Asn Asn Glu Glu Arg Leu Gln Ala Arg Ile Val Thr Ala Leu Ile
                165                 170                 175

ggc tgg gca cta tcg agt gtt gcc ttc atg aag ctc ggc tcc atc agc   576
Gly Trp Ala Leu Ser Ser Val Ala Phe Met Lys Leu Gly Ser Ile Ser
            180                 185                 190

ggc atg ctt aac ctg ctg cac gtc acc gaa gat gga aac acc act ttg   624
Gly Met Leu Asn Leu Leu His Val Thr Glu Asp Gly Asn Thr Thr Leu
        195                 200                 205

gat gtc tcc aac ctt gat gaa ctg ttg att cca cga tct gcc gaa gat   672
Asp Val Ser Asn Leu Asp Glu Leu Leu Ile Pro Arg Ser Ala Glu Asp
    210                 215                 220

gac gag ctg gtc cag caa gac ctc cac gac acg ttc tcc gcg ctt cag   720
Asp Glu Leu Val Gln Gln Asp Leu His Asp Thr Phe Ser Ala Leu Gln
225                 230                 235                 240

cga ttt gca gcg cgc ggg ctg gat tcc agg ttc cct gag gtg gca cga   768
Arg Phe Ala Ala Arg Gly Leu Asp Ser Arg Phe Pro Glu Val Ala Arg
                245                 250                 255

ttc gca gac gac gtg gtg cgt ttg ttc ctc aaa aat gac tagctgaaga    817
Phe Ala Asp Asp Val Val Arg Leu Phe Leu Lys Asn Asp
            260                 265

gcaccggttg ctt                                                   830


<210> 2910
<211> 269
<212> PRT
<213> Corynebacterium glutamicum

<400> 2910
Ile Leu Arg Asn Leu Gly Gln Ser Leu Gly Ser Leu His Ala Ala Thr
  1               5                  10                  15

Ala Asp Arg Glu Glu Asp Phe Asn Ile Leu Leu Asn Arg Met Leu Ala
             20                  25                  30

Lys Tyr Pro Ala Thr Ala Glu Met Gln Lys Asn Arg Asp Arg Leu Leu
         35                  40                  45
```

```
Pro Ala Ala Ile Glu Val Gly Lys Lys Ile Leu Val Asp Ala Gly Val
     50                  55                  60

Thr Val Pro Glu Val Val Glu Glu Phe Ala Arg Val Ala Arg Arg Arg
 65                  70                  75                  80

Leu Ile Ser Gly Arg His Arg Ala Phe Thr Pro Phe Asp Leu Ser Pro
                 85                  90                  95

Asp Asn Ile Ile Val Ala Glu Arg Thr His Phe Leu Asp Tyr Glu Val
            100                 105                 110

Ala Gly Phe Arg Asp Ala Thr Phe Asp Val Ala Cys Val Ile Ala Gly
        115                 120                 125

Phe Pro Gln Phe Val Phe Ser Arg Pro Ile Ser Asp Asp Glu Val Asp
    130                 135                 140

Glu Leu Ile Glu Ser Trp Val Gln Glu Val Arg Gly Ile Trp Pro Asn
145                 150                 155                 160

Val Asn Asn Glu Glu Arg Leu Gln Ala Arg Ile Val Thr Ala Leu Ile
                165                 170                 175

Gly Trp Ala Leu Ser Ser Val Ala Phe Met Lys Leu Gly Ser Ile Ser
            180                 185                 190

Gly Met Leu Asn Leu Leu His Val Thr Glu Asp Gly Asn Thr Thr Leu
        195                 200                 205

Asp Val Ser Asn Leu Asp Glu Leu Leu Ile Pro Arg Ser Ala Glu Asp
    210                 215                 220

Asp Glu Leu Val Gln Gln Asp Leu His Asp Thr Phe Ser Ala Leu Gln
225                 230                 235                 240

Arg Phe Ala Ala Arg Gly Leu Asp Ser Arg Phe Pro Glu Val Ala Arg
                245                 250                 255

Phe Ala Asp Asp Val Val Arg Leu Phe Leu Lys Asn Asp
            260                 265
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<210> 2911
<211> 669
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(646)
<223> RXA02789

<400> 2911
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ttcttaacac taaacaatgg aaaggtaagc gggtttttct atg aag gtt tcc gcc 115
                                              Met Lys Val Ser Ala
                                                1   5

gat aca ccc ggt cac gat gat cca ggc cca ggc cgg cgc ctt ggc tta 163

```
Asp Thr Pro Gly His Asp Asp Pro Gly Pro Gly Arg Arg Leu Gly Leu
                10                  15                  20

gat gtc ggc acc gtg cgc atc gga gtg gca gcc tct gac cgc gat gcc   211
Asp Val Gly Thr Val Arg Ile Gly Val Ala Ala Ser Asp Arg Asp Ala
            25                  30                  35

aag ctt gcc atg cct gtg gaa acc gtt ccg cgg gaa act gga ttc aaa   259
Lys Leu Ala Met Pro Val Glu Thr Val Pro Arg Glu Thr Gly Phe Lys
        40                  45                  50

ggg cca gac ctg gcc gat att gat cgg ttg gtc gcc atc gtt gag gaa   307
Gly Pro Asp Leu Ala Asp Ile Asp Arg Leu Val Ala Ile Val Glu Glu
    55                  60                  65

tac aac gcc gtg gaa gtc att gtt ggt cta ccc aca gat ctg cag gga   355
Tyr Asn Ala Val Glu Val Ile Val Gly Leu Pro Thr Asp Leu Gln Gly
70                  75                  80                  85

aat ggc tcc gcc agt gtg aag cat gca aag gaa att gct ttc cgc gtc   403
Asn Gly Ser Ala Ser Val Lys His Ala Lys Glu Ile Ala Phe Arg Val
                90                  95                  100

cgt cgg cgc ctc acc aat gct gga aag aac att ccg gta cgg ctt ggc   451
Arg Arg Arg Leu Thr Asn Ala Gly Lys Asn Ile Pro Val Arg Leu Gly
            105                 110                 115

gac gaa cgc ctc acc acc gtc gtg gcc acc caa gcc ttg cgg gcc tca   499
Asp Glu Arg Leu Thr Thr Val Val Ala Thr Gln Ala Leu Arg Ala Ser
        120                 125                 130

gga gtc agc gaa aaa gcg gga cgt aaa gtt att gat caa gct gcc gca   547
Gly Val Ser Glu Lys Ala Gly Arg Lys Val Ile Asp Gln Ala Ala Ala
    135                 140                 145

gta gaa atc ctt caa acc tgg ttg gat gct cgc acc cga gcc ctt gaa   595
Val Glu Ile Leu Gln Thr Trp Leu Asp Ala Arg Thr Arg Ala Leu Glu
150                 155                 160                 165

cca caa tcc aca gac acc caa gat ttc gac gag aag gga aat ttc cca   643
Pro Gln Ser Thr Asp Thr Gln Asp Phe Asp Glu Lys Gly Asn Phe Pro
                170                 175                 180

gga tgaaccaaat ccgaaaccgc cgg                                    669
Gly
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<210> 2912
<211> 182
<212> PRT
<213> Corynebacterium glutamicum

<400> 2912

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Met Lys Val Ser Ala Asp Thr Pro Gly His Asp Asp Pro Gly Pro Gly
  1               5                  10                  15

Arg Arg Leu Gly Leu Asp Val Gly Thr Val Arg Ile Gly Val Ala Ala
            20                  25                  30

Ser Asp Arg Asp Ala Lys Leu Ala Met Pro Val Glu Thr Val Pro Arg
```

```
         35                  40                  45

Glu Thr Gly Phe Lys Gly Pro Asp Leu Ala Asp Ile Asp Arg Leu Val
     50                  55                  60

Ala Ile Val Glu Glu Tyr Asn Ala Val Glu Val Ile Val Gly Leu Pro
 65                  70                  75                  80

Thr Asp Leu Gln Gly Asn Gly Ser Ala Ser Val Lys His Ala Lys Glu
                 85                  90                  95

Ile Ala Phe Arg Val Arg Arg Arg Leu Thr Asn Ala Gly Lys Asn Ile
            100                 105                 110

Pro Val Arg Leu Gly Asp Glu Arg Leu Thr Thr Val Val Ala Thr Gln
        115                 120                 125

Ala Leu Arg Ala Ser Gly Val Ser Glu Lys Ala Gly Arg Lys Val Ile
    130                 135                 140

Asp Gln Ala Ala Ala Val Glu Ile Leu Gln Thr Trp Leu Asp Ala Arg
145                 150                 155                 160

Thr Arg Ala Leu Glu Pro Gln Ser Thr Asp Thr Gln Asp Phe Asp Glu
                165                 170                 175

Lys Gly Asn Phe Pro Gly
            180


<210> 2913
<211> 825
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(802)
<223> RXA02793

<400> 2913
tgcatgctcc tctagtgatg tggtggaaag tcaagggata accgttgaaa actgtggctc 60

ggtggtgaat tttgatagtc caccatcaca catcgccttg atg aaa agc gcc gcc   115
                                            Met Lys Ser Ala Ala
                                              1               5

gta ccc acg ctt gat gct tta ggt gtt ttg gat cgc gtg gtg acc aaa   163
Val Pro Thr Leu Asp Ala Leu Gly Val Leu Asp Arg Val Val Thr Lys
                 10                  15                  20

gct ggt gcc ttc cca gct ggg tat tac gac gcc gat tta tcg gaa aga   211
Ala Gly Ala Phe Pro Ala Gly Tyr Tyr Asp Ala Asp Leu Ser Glu Arg
             25                  30                  35

gtc acg gac atc cca acg ctg tcc aac aag atc gac gcc agc gga cac   259
Val Thr Asp Ile Pro Thr Leu Ser Asn Lys Ile Asp Ala Ser Gly His
         40                  45                  50

gtg ttg atc tcg aaa gaa gtc gtt gtt gcc gcc aac cca gac att gtt   307
Val Leu Ile Ser Lys Glu Val Val Val Ala Ala Asn Pro Asp Ile Val
```

55 60 65

ttc ggc gaa act gac acc atc aac cgc gca tcc atg gca tcc tcg aac 355
Phe Gly Glu Thr Asp Thr Ile Asn Arg Ala Ser Met Ala Ser Ser Asn
70 75 80 85

atc ccg gtc gtg gag gaa cca gca ttc tgt ggc agc atc gac ggc gac 403
Ile Pro Val Val Glu Glu Pro Ala Phe Cys Gly Ser Ile Asp Gly Asp
90 95 100

gtg agt ttt gat gat gtc tgg tca caa atc tcc acc tat ggc acc att 451
Val Ser Phe Asp Asp Val Trp Ser Gln Ile Ser Thr Tyr Gly Thr Ile
105 110 115

ttt gat cgc tcg aca gaa gca gac gca tac att gca acg ttg aag gaa 499
Phe Asp Arg Ser Thr Glu Ala Asp Ala Tyr Ile Ala Thr Leu Lys Glu
120 125 130

cgt gtt tct gaa gta tcc tcg cgg gtt act gac tcc gga aaa act gtg 547
Arg Val Ser Glu Val Ser Ser Arg Val Thr Asp Ser Gly Lys Thr Val
135 140 145

gcg gtg ctc tac ccc acc atc ggc ggc gga gtc acc tac gca tac ggc 595
Ala Val Leu Tyr Pro Thr Ile Gly Gly Gly Val Thr Tyr Ala Tyr Gly
150 155 160 165

cgc gga tcc atg gcc aac cca ctt gtt gcc gaa gca ggc ctg acc aac 643
Arg Gly Ser Met Ala Asn Pro Leu Val Ala Glu Ala Gly Leu Thr Asn
170 175 180

gtt ttc gca gac caa tcc gaa cgc gtc ttt gag gtc acg gca gaa gaa 691
Val Phe Ala Asp Gln Ser Glu Arg Val Phe Glu Val Thr Ala Glu Glu
185 190 195

ctg atc tcc gaa acc ccg act cat cat cgt ttt aca cag cga cgg ttc 739
Leu Ile Ser Glu Thr Pro Thr His His Arg Phe Thr Gln Arg Arg Phe
200 205 210

ccc ttc aga cat cgt cgc aga ggt ggg caa tct cca agg gtc cag cgc 787
Pro Phe Arg His Arg Arg Arg Gly Gly Gln Ser Pro Arg Val Gln Arg
215 220 225

act cac tgc tct gag tgagaacaaa gtgctgccca tac 825
Thr His Cys Ser Glu
230

<210> 2914
<211> 234
<212> PRT
<213> Corynebacterium glutamicum

<400> 2914
Met Lys Ser Ala Ala Val Pro Thr Leu Asp Ala Leu Gly Val Leu Asp
1 5 10 15

Arg Val Val Thr Lys Ala Gly Ala Phe Pro Ala Gly Tyr Tyr Asp Ala
20 25 30

Asp Leu Ser Glu Arg Val Thr Asp Ile Pro Thr Leu Ser Asn Lys Ile
35 40 45

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Asp Ala Ser Gly His Val Leu Ile Ser Lys Glu Val Val Val Ala Ala
     50                  55                  60

Asn Pro Asp Ile Val Phe Gly Glu Thr Asp Thr Ile Asn Arg Ala Ser
 65                  70                  75                  80

Met Ala Ser Ser Asn Ile Pro Val Val Glu Glu Pro Ala Phe Cys Gly
                 85                  90                  95

Ser Ile Asp Gly Asp Val Ser Phe Asp Asp Val Trp Ser Gln Ile Ser
            100                 105                 110

Thr Tyr Gly Thr Ile Phe Asp Arg Ser Thr Glu Ala Asp Ala Tyr Ile
        115                 120                 125

Ala Thr Leu Lys Glu Arg Val Ser Glu Val Ser Ser Arg Val Thr Asp
    130                 135                 140

Ser Gly Lys Thr Val Ala Val Leu Tyr Pro Thr Ile Gly Gly Gly Val
145                 150                 155                 160

Thr Tyr Ala Tyr Gly Arg Gly Ser Met Ala Asn Pro Leu Val Ala Glu
                165                 170                 175

Ala Gly Leu Thr Asn Val Phe Ala Asp Gln Ser Glu Arg Val Phe Glu
            180                 185                 190

Val Thr Ala Glu Glu Leu Ile Ser Glu Thr Pro Thr His His Arg Phe
        195                 200                 205

Thr Gln Arg Arg Phe Pro Phe Arg His Arg Arg Arg Gly Gly Gln Ser
    210                 215                 220

Pro Arg Val Gln Arg Thr His Cys Ser Glu
225                 230
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<210> 2915
<211> 672
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(649)
<223> RXA02796

<400> 2915
gattattcat ggaacatcct tagcggagtt atgcaaacgt tttcataagg ggttattcca 60

ttctacgtcg atctttgtag aaggtggtta ttatggcttc atg aga ctg ttc gcg 115
                                            Met Arg Leu Phe Ala
                                              1   5

tct atc act ccg ccg att gaa gtc acc gag cat ctg atc aac gcg ctt 163
Ser Ile Thr Pro Pro Ile Glu Val Thr Glu His Leu Ile Asn Ala Leu
                10   15   20

cgt ccc tac aag gat gat ctg cgg tgg tct gat cca gac aat tgg cac 211
Arg Pro Tyr Lys Asp Asp Leu Arg Trp Ser Asp Pro Asp Asn Trp His

```
            25                  30                  35

atc acg ttg gcg ttc tat gga gaa tta cct gat ggg gca gtc gaa gat   259
Ile Thr Leu Ala Phe Tyr Gly Glu Leu Pro Asp Gly Ala Val Glu Asp
        40                  45                  50

ctc att gag cat ctg aca agt gca gcc cga atc aat gaa gaa ttc acc   307
Leu Ile Glu His Leu Thr Ser Ala Ala Arg Ile Asn Glu Glu Phe Thr
    55                  60                  65

atc aga atc aaa ggc gca ggc tca ttt aat cgg aag aat ttg tgg atg   355
Ile Arg Ile Lys Gly Ala Gly Ser Phe Asn Arg Lys Asn Leu Trp Met
70                  75                  80                  85

ggt gtt ggt ggt gac acc aaa gat ctg cgg cga ctg atg gct gat tgt   403
Gly Val Gly Gly Asp Thr Lys Asp Leu Arg Arg Leu Met Ala Asp Cys
                90                  95                  100

ctg att gat cct gag gaa cgc cga cgc cag cgt gca cac ctg acc gtg   451
Leu Ile Asp Pro Glu Glu Arg Arg Arg Gln Arg Ala His Leu Thr Val
            105                 110                 115

gcg aaa cca acg cag cga cag cgc agc cgc gat tgg gat cct gtc atc   499
Ala Lys Pro Thr Gln Arg Gln Arg Ser Arg Asp Trp Asp Pro Val Ile
        120                 125                 130

ccc gat ctg gtc cac gct ctc tct ata tac gaa ggc ccc gaa tgg cca   547
Pro Asp Leu Val His Ala Leu Ser Ile Tyr Glu Gly Pro Glu Trp Pro
    135                 140                 145

gtc gat gag att gaa ctg gtg tct tct gaa cct gga aaa ggc aga agc   595
Val Asp Glu Ile Glu Leu Val Ser Ser Glu Pro Gly Lys Gly Arg Ser
150                 155                 160                 165

ggt ggg cca ctg tat aca acc gtg gcc acc att gcg ttg tca tct gcg   643
Gly Gly Pro Leu Tyr Thr Thr Val Ala Thr Ile Ala Leu Ser Ser Ala
                170                 175                 180

ctg gtt taaaggctca accgcggaac ggc                                672
Leu Val
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<210> 2916
<211> 183
<212> PRT
<213> Corynebacterium glutamicum

<400> 2916

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Met Arg Leu Phe Ala Ser Ile Thr Pro Pro Ile Glu Val Thr Glu His
  1               5                  10                  15

Leu Ile Asn Ala Leu Arg Pro Tyr Lys Asp Asp Leu Arg Trp Ser Asp
             20                  25                  30

Pro Asp Asn Trp His Ile Thr Leu Ala Phe Tyr Gly Glu Leu Pro Asp
         35                  40                  45

Gly Ala Val Glu Asp Leu Ile Glu His Leu Thr Ser Ala Ala Arg Ile
     50                  55                  60
```

```
Asn Glu Glu Phe Thr Ile Arg Ile Lys Gly Ala Gly Ser Phe Asn Arg
 65                  70                  75                  80

Lys Asn Leu Trp Met Gly Val Gly Gly Asp Thr Lys Asp Leu Arg Arg
                 85                  90                  95

Leu Met Ala Asp Cys Leu Ile Asp Pro Glu Glu Arg Arg Arg Gln Arg
            100                 105                 110

Ala His Leu Thr Val Ala Lys Pro Thr Gln Arg Gln Arg Ser Arg Asp
        115                 120                 125

Trp Asp Pro Val Ile Pro Asp Leu Val His Ala Leu Ser Ile Tyr Glu
    130                 135                 140

Gly Pro Glu Trp Pro Val Asp Glu Ile Glu Leu Val Ser Ser Glu Pro
145                 150                 155                 160

Gly Lys Gly Arg Ser Gly Gly Pro Leu Tyr Thr Thr Val Ala Thr Ile
                165                 170                 175

Ala Leu Ser Ser Ala Leu Val
            180
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<210> 2917
<211> 1548
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1525)
<223> RXA02798

<400> 2917

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gcatcaaaat catgtgcatt catcattgct gatcatcata gacctgttgg caaatgaatt 60

caccaattct ttaaagctct caccctcttt agggaactga atg cgg tct gta ctc   115
                                              Met Arg Ser Val Leu
                                                1               5

gac tac tgg atc atg act ctt gca cct tcc acc aat gcg gtt tcg cag   163
Asp Tyr Trp Ile Met Thr Leu Ala Pro Ser Thr Asn Ala Val Ser Gln
                10                  15                  20

caa aca aga agg aac cct tcc caa gcg ccg cga ctt ctt cat cga ctt   211
Gln Thr Arg Arg Asn Pro Ser Gln Ala Pro Arg Leu Leu His Arg Leu
            25                  30                  35

cac ttc ttt gcc ggc att atc tgc gca ccg ttg att ttc atc gct gcg   259
His Phe Phe Ala Gly Ile Ile Cys Ala Pro Leu Ile Phe Ile Ala Ala
        40                  45                  50

ctc acc gga ctg gtg tat gcg ttc tcc ccc acc att gaa agc atc tct   307
Leu Thr Gly Leu Val Tyr Ala Phe Ser Pro Thr Ile Glu Ser Ile Ser
    55                  60                  65

aat cag gaa atg ctc acg gtc tcc aag tcg gct agc gac aca gct ctt   355
Asn Gln Glu Met Leu Thr Val Ser Lys Ser Ala Ser Asp Thr Ala Leu
70                  75                  80                  85
```

```
ccg gtg cgt gaa caa gtg agc atc gcc caa gaa ctc cac ccc gat tta   403
Pro Val Arg Glu Gln Val Ser Ile Ala Gln Glu Leu His Pro Asp Leu
                 90                  95                 100

gat ctc tca ggt gtc cgg ctt ggc gat gat tcc tcc acc acc cgc gtc   451
Asp Leu Ser Gly Val Arg Leu Gly Asp Asp Ser Ser Thr Thr Arg Val
            105                 110                 115

ctc ttc gcc gac gag acg ctt gct gaa tcc aca gtc cgc gcc gtg ttt   499
Leu Phe Ala Asp Glu Thr Leu Ala Glu Ser Thr Val Arg Ala Val Phe
        120                 125                 130

gtt gat ccc tac acc ggc gag atc acc ggt gat acc acc caa tac gga   547
Val Asp Pro Tyr Thr Gly Glu Ile Thr Gly Asp Thr Thr Gln Tyr Gly
    135                 140                 145

agc tca gct gca ctg ccg ttt cgg caa tgg gtc tcg caa ggt cac cgc   595
Ser Ser Ala Ala Leu Pro Phe Arg Gln Trp Val Ser Gln Gly His Arg
150                 155                 160                 165

atg ttg tgg ctt ggt gaa cct gga cgt att tat tcc gaa ctt gcg gca   643
Met Leu Trp Leu Gly Glu Pro Gly Arg Ile Tyr Ser Glu Leu Ala Ala
                170                 175                 180

agt tgg ctc gga gtt tta gcc gta ggc ggt ttc gca tta ttg tgg ttg   691
Ser Trp Leu Gly Val Leu Ala Val Gly Gly Phe Ala Leu Leu Trp Leu
            185                 190                 195

cgc aac aaa aag ccc ggc cgc ttg aga aag atg gtg cga act ggt ggc   739
Arg Asn Lys Lys Pro Gly Arg Leu Arg Lys Met Val Arg Thr Gly Gly
        200                 205                 210

cgt ggt cga gtg aaa acg tat cgc cga cat gca gca ttg ggc acc gta   787
Arg Gly Arg Val Lys Thr Tyr Arg Arg His Ala Ala Leu Gly Thr Val
    215                 220                 225

gcg ggc ttg ggt ttt gtg ttc ctc acc ttt act ggc ctg acc tgg tca   835
Ala Gly Leu Gly Phe Val Phe Leu Thr Phe Thr Gly Leu Thr Trp Ser
230                 235                 240                 245

act tat gcg gga tcc aac atc acg gat tta cgc acc caa ctc aat tgg   883
Thr Tyr Ala Gly Ser Asn Ile Thr Asp Leu Arg Thr Gln Leu Asn Trp
                250                 255                 260

acg cag cct tcc gtt aac gct tct cta aca gct gcc cca caa gtg gac   931
Thr Gln Pro Ser Val Asn Ala Ser Leu Thr Ala Ala Pro Gln Val Asp
            265                 270                 275

atg cat gat gaa cac gca ggt cat cac atg cat atg gag tcg gca acc   979
Met His Asp Glu His Ala Gly His His Met His Met Glu Ser Ala Thr
        280                 285                 290

tca ggc tca ggt tct ata gat ctg gta gcg gcc acg gct atc tcc gaa  1027
Ser Gly Ser Gly Ser Ile Asp Leu Val Ala Ala Thr Ala Ile Ser Glu
    295                 300                 305

tta cgc act ccc ctc acc att act ccc cca gca caa gat ggc ctc gcg  1075
Leu Arg Thr Pro Leu Thr Ile Thr Pro Pro Ala Gln Asp Gly Leu Ala
310                 315                 320                 325
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tgg act gcc aca gaa aac cgc gac gcc tac cga ttc acc act gac acc   1123
Trp Thr Ala Thr Glu Asn Arg Asp Ala Tyr Arg Phe Thr Thr Asp Thr
                330                 335                 340

atc gct gtt gat ggc gac acc gga atg ctg acc aac cgt ttg aat tcc   1171
Ile Ala Val Asp Gly Asp Thr Gly Met Leu Thr Asn Arg Leu Asn Ser
            345                 350                 355

act gat tgg cca tta gct gct caa gcg agt gca tgg ctc atc cag ctt   1219
Thr Asp Trp Pro Leu Ala Ala Gln Ala Ser Ala Trp Leu Ile Gln Leu
        360                 365                 370

cac atg ggc acc ctg ttt ggc ctt ccc aac cag gtt gta ctt ggg ctg   1267
His Met Gly Thr Leu Phe Gly Leu Pro Asn Gln Val Val Leu Gly Leu
    375                 380                 385

ttg gct gcc tca ata atc gtg atg atc ggc ctt ggg tat tgg atg ctg   1315
Leu Ala Ala Ser Ile Ile Val Met Ile Gly Leu Gly Tyr Trp Met Leu
390                 395                 400                 405

tgg cag cat cgg cca cgg gaa ggt tgg cct agc gct ccc aag cgt gca   1363
Trp Gln His Arg Pro Arg Glu Gly Trp Pro Ser Ala Pro Lys Arg Ala
                410                 415                 420

gga ttt gaa aaa ccc acc tgg gga act atc gcg ttg ggt gtt gtg gtg   1411
Gly Phe Glu Lys Pro Thr Trp Gly Thr Ile Ala Leu Gly Val Val Val
            425                 430                 435

atc gcg tat ggg ctt ctc gcg cca ctt ttt gca gtt tca ctg ctc gtg   1459
Ile Ala Tyr Gly Leu Leu Ala Pro Leu Phe Ala Val Ser Leu Leu Val
        440                 445                 450

ttt att gga tta agc ctt gga gtg cgg ttt att tct cgt atg tcc ggg   1507
Phe Ile Gly Leu Ser Leu Gly Val Arg Phe Ile Ser Arg Met Ser Gly
    455                 460                 465

cgc gcg gac acg tcc aac taagaacacc aaaccacacc gcc                 1548
Arg Ala Asp Thr Ser Asn
470                 475
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<210> 2918
<211> 475
<212> PRT
<213> Corynebacterium glutamicum

<400> 2918

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Met Arg Ser Val Leu Asp Tyr Trp Ile Met Thr Leu Ala Pro Ser Thr
  1               5                  10                  15

Asn Ala Val Ser Gln Gln Thr Arg Arg Asn Pro Ser Gln Ala Pro Arg
             20                  25                  30

Leu Leu His Arg Leu His Phe Phe Ala Gly Ile Ile Cys Ala Pro Leu
         35                  40                  45

Ile Phe Ile Ala Ala Leu Thr Gly Leu Val Tyr Ala Phe Ser Pro Thr
     50                  55                  60

Ile Glu Ser Ile Ser Asn Gln Glu Met Leu Thr Val Ser Lys Ser Ala
 65                  70                  75                  80
```

```
Ser Asp Thr Ala Leu Pro Val Arg Glu Gln Val Ser Ile Ala Gln Glu
                 85                  90                  95

Leu His Pro Asp Leu Asp Leu Ser Gly Val Arg Leu Gly Asp Asp Ser
            100                 105                 110

Ser Thr Thr Arg Val Leu Phe Ala Asp Glu Thr Leu Ala Glu Ser Thr
        115                 120                 125

Val Arg Ala Val Phe Val Asp Pro Tyr Thr Gly Glu Ile Thr Gly Asp
    130                 135                 140

Thr Thr Gln Tyr Gly Ser Ser Ala Ala Leu Pro Phe Arg Gln Trp Val
145                 150                 155                 160

Ser Gln Gly His Arg Met Leu Trp Leu Gly Glu Pro Gly Arg Ile Tyr
                165                 170                 175

Ser Glu Leu Ala Ala Ser Trp Leu Gly Val Leu Ala Val Gly Gly Phe
            180                 185                 190

Ala Leu Leu Trp Leu Arg Asn Lys Lys Pro Gly Arg Leu Arg Lys Met
        195                 200                 205

Val Arg Thr Gly Gly Arg Gly Arg Val Lys Thr Tyr Arg Arg His Ala
    210                 215                 220

Ala Leu Gly Thr Val Ala Gly Leu Gly Phe Val Phe Leu Thr Phe Thr
225                 230                 235                 240

Gly Leu Thr Trp Ser Thr Tyr Ala Gly Ser Asn Ile Thr Asp Leu Arg
                245                 250                 255

Thr Gln Leu Asn Trp Thr Gln Pro Ser Val Asn Ala Ser Leu Thr Ala
            260                 265                 270

Ala Pro Gln Val Asp Met His Asp Glu His Ala Gly His His Met His
        275                 280                 285

Met Glu Ser Ala Thr Ser Gly Ser Gly Ser Ile Asp Leu Val Ala Ala
    290                 295                 300

Thr Ala Ile Ser Glu Leu Arg Thr Pro Leu Thr Ile Thr Pro Pro Ala
305                 310                 315                 320

Gln Asp Gly Leu Ala Trp Thr Ala Thr Glu Asn Arg Asp Ala Tyr Arg
                325                 330                 335

Phe Thr Thr Asp Thr Ile Ala Val Asp Gly Asp Thr Gly Met Leu Thr
            340                 345                 350

Asn Arg Leu Asn Ser Thr Asp Trp Pro Leu Ala Ala Gln Ala Ser Ala
        355                 360                 365

Trp Leu Ile Gln Leu His Met Gly Thr Leu Phe Gly Leu Pro Asn Gln
    370                 375                 380

Val Val Leu Gly Leu Leu Ala Ala Ser Ile Ile Val Met Ile Gly Leu
385                 390                 395                 400
```

```
Gly Tyr Trp Met Leu Trp Gln His Arg Pro Arg Glu Gly Trp Pro Ser
                405                 410                 415

Ala Pro Lys Arg Ala Gly Phe Glu Lys Pro Thr Trp Gly Thr Ile Ala
            420                 425                 430

Leu Gly Val Val Val Ile Ala Tyr Gly Leu Leu Ala Pro Leu Phe Ala
        435                 440                 445

Val Ser Leu Leu Val Phe Ile Gly Leu Ser Leu Gly Val Arg Phe Ile
    450                 455                 460

Ser Arg Met Ser Gly Arg Ala Asp Thr Ser Asn
465                 470                 475


<210> 2919
<211> 396
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(373)
<223> RXA02799

<400> 2919
tcgcgcgcaa gtgttcagta atatggactc ccagtaacgg gttttcatga cgcgttaaat 60

tttttagttg atcacagata caccaatcag gagtagcgca gtg gca cgc aac att   115
                                            Val Ala Arg Asn Ile
                                              1               5

gaa gac atc cag cgc gat att gag cgc acc cgc cgt cag ttg gct tcc   163
Glu Asp Ile Gln Arg Asp Ile Glu Arg Thr Arg Arg Gln Leu Ala Ser
                  10                  15                  20

acc ctc gac gag ctg gca gac cgc agc aag cct tcc aac ttg gtc gat   211
Thr Leu Asp Glu Leu Ala Asp Arg Ser Lys Pro Ser Asn Leu Val Asp
              25                  30                  35

gac gcc aag aac cag gca acc gcg aag ctg cag gaa tca aac gta cag   259
Asp Ala Lys Asn Gln Ala Thr Ala Lys Leu Gln Glu Ser Asn Val Gln
          40                  45                  50

aag gtg ctc ctg ggc gtc gct gct gtc gtc gtc ggt gct gtt gta ttc   307
Lys Val Leu Leu Gly Val Ala Ala Val Val Val Gly Ala Val Val Phe
      55                  60                  65

agc gtt gtg cgt ggc cgt aag aag gca aac gat ctg aag gaa atc cag   355
Ser Val Val Arg Gly Arg Lys Lys Ala Asn Asp Leu Lys Glu Ile Gln
  70                  75                  80                  85

cgc ctg ctc tcc gag cgt taaattgctt ttcgacgggg cgt                396
Arg Leu Leu Ser Glu Arg
                90


<210> 2920
<211> 91
<212> PRT
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<213> Corynebacterium glutamicum

<400> 2920

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Val Ala Arg Asn Ile Glu Asp Ile Gln Arg Asp Ile Glu Arg Thr Arg
  1               5                  10                  15

Arg Gln Leu Ala Ser Thr Leu Asp Glu Leu Ala Asp Arg Ser Lys Pro
             20                  25                  30

Ser Asn Leu Val Asp Asp Ala Lys Asn Gln Ala Thr Ala Lys Leu Gln
         35                  40                  45

Glu Ser Asn Val Gln Lys Val Leu Leu Gly Val Ala Ala Val Val Val
     50                  55                  60

Gly Ala Val Val Phe Ser Val Val Arg Gly Arg Lys Lys Ala Asn Asp
 65                  70                  75                  80

Leu Lys Glu Ile Gln Arg Leu Leu Ser Glu Arg
                 85                  90
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<210> 2921
<211> 552
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(552)
<223> RXA02815

<400> 2921

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tgg ctg cgc agt acc aaa gag ttc gaa gac cag ccc gtg att ccg gca   48
Trp Leu Arg Ser Thr Lys Glu Phe Glu Asp Gln Pro Val Ile Pro Ala
  1               5                  10                  15

ttc gaa gta atc gca acg gtt gcc tct gaa ttc gca ggc gac gac ggc   96
Phe Glu Val Ile Ala Thr Val Ala Ser Glu Phe Ala Gly Asp Asp Gly
             20                  25                  30

aac tac tcc aac gaa ttc ccc gtg gaa gat cta gtc gga tac gtt gac   144
Asn Tyr Ser Asn Glu Phe Pro Val Glu Asp Leu Val Gly Tyr Val Asp
         35                  40                  45

gcc atc acc gaa gcc ggc gga tac gca gtc ctg gat ctt caa ccc gga   192
Ala Ile Thr Glu Ala Gly Gly Tyr Ala Val Leu Asp Leu Gln Pro Gly
     50                  55                  60

cgc gcc aac ttc ctc gac caa gcc aaa atg tat gaa gaa ctc ctc aaa   240
Arg Ala Asn Phe Leu Asp Gln Ala Lys Met Tyr Glu Glu Leu Leu Lys
 65                  70                  75                  80

cga cca aac gtt gga ttg gcg cta gat ccc gag tgg aaa atc gga ccc   288
Arg Pro Asn Val Gly Leu Ala Leu Asp Pro Glu Trp Lys Ile Gly Pro
                 85                  90                  95

gat gag caa ccc atg aca cga gtg ggc tct gca gat gcc gcc gaa atc   336
Asp Glu Gln Pro Met Thr Arg Val Gly Ser Ala Asp Ala Ala Glu Ile
            100                 105                 110
```

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aac gaa gta tcc cag tgg ctc gcc gac ctg acc gcc gag aac gat ctt   384
Asn Glu Val Ser Gln Trp Leu Ala Asp Leu Thr Ala Glu Asn Asp Leu
        115                 120                 125

cca caa aag gca ttt gta ctg cac caa ttc caa ttg gaa atg ctc acc   432
Pro Gln Lys Ala Phe Val Leu His Gln Phe Gln Leu Glu Met Leu Thr
    130                 135                 140

aat cgg gat caa atc aat acc gat cac ctg gaa ctg gct gtc gtg ttg   480
Asn Arg Asp Gln Ile Asn Thr Asp His Leu Glu Leu Ala Val Val Leu
145                 150                 155                 160

cac gca gat gga cac gga aac gca ggg gat aag tac gca act tgg aac   528
His Ala Asp Gly His Gly Asn Ala Gly Asp Lys Tyr Ala Thr Trp Asn
                165                 170                 175

atg ctt cgc gag gga ctg agc ccg                                  552
Met Leu Arg Glu Gly Leu Ser Pro
            180
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<210> 2922
<211> 184
<212> PRT
<213> Corynebacterium glutamicum

<400> 2922

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Trp Leu Arg Ser Thr Lys Glu Phe Glu Asp Gln Pro Val Ile Pro Ala
  1               5                  10                  15

Phe Glu Val Ile Ala Thr Val Ala Ser Glu Phe Ala Gly Asp Asp Gly
             20                  25                  30

Asn Tyr Ser Asn Glu Phe Pro Val Glu Asp Leu Val Gly Tyr Val Asp
         35                  40                  45

Ala Ile Thr Glu Ala Gly Gly Tyr Ala Val Leu Asp Leu Gln Pro Gly
     50                  55                  60

Arg Ala Asn Phe Leu Asp Gln Ala Lys Met Tyr Glu Glu Leu Leu Lys
 65                  70                  75                  80

Arg Pro Asn Val Gly Leu Ala Leu Asp Pro Glu Trp Lys Ile Gly Pro
                 85                  90                  95

Asp Glu Gln Pro Met Thr Arg Val Gly Ser Ala Asp Ala Ala Glu Ile
            100                 105                 110

Asn Glu Val Ser Gln Trp Leu Ala Asp Leu Thr Ala Glu Asn Asp Leu
        115                 120                 125

Pro Gln Lys Ala Phe Val Leu His Gln Phe Gln Leu Glu Met Leu Thr
    130                 135                 140

Asn Arg Asp Gln Ile Asn Thr Asp His Leu Glu Leu Ala Val Val Leu
145                 150                 155                 160

His Ala Asp Gly His Gly Asn Ala Gly Asp Lys Tyr Ala Thr Trp Asn
                165                 170                 175

Met Leu Arg Glu Gly Leu Ser Pro
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180

<210> 2923
<211> 370
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(370)
<223> RXA02823

<400> 2923
ttatgtntnt aaacagccag ttgggggtca tgggggagcg ccccgtgact ggttaatgcc 60

ccgatctggg acgtacagta acaacgacac tggaggtgcc atg act gtt aga aat 115
Met Thr Val Arg Asn
1 5

ccc gac cgt gag gca atc cgt cac gga aaa att acg acg gag gcg ctg 163
Pro Asp Arg Glu Ala Ile Arg His Gly Lys Ile Thr Thr Glu Ala Leu
10 15 20

cgt gag cgt ccc gca tac ccg acc tgg gca atg aag ctg acc atg gcc 211
Arg Glu Arg Pro Ala Tyr Pro Thr Trp Ala Met Lys Leu Thr Met Ala
25 30 35

atc act ggc cta atg ttt ggt ggc ttc gtt ctt gtt cac atg atc gga 259
Ile Thr Gly Leu Met Phe Gly Gly Phe Val Leu Val His Met Ile Gly
40 45 50

aac ctg aaa atc ttc atg ccg gac tac gca gcc gat tct gcg cat ccg 307
Asn Leu Lys Ile Phe Met Pro Asp Tyr Ala Ala Asp Ser Ala His Pro
55 60 65

ggt gaa gca caa gta gat gtc tac ggc gag ttc ctg cgt gag atc gga 355
Gly Glu Ala Gln Val Asp Val Tyr Gly Glu Phe Leu Arg Glu Ile Gly
70 75 80 85

tcc ccg atc ctc cca 370
Ser Pro Ile Leu Pro
90

<210> 2924
<211> 90
<212> PRT
<213> Corynebacterium glutamicum

<400> 2924
Met Thr Val Arg Asn Pro Asp Arg Glu Ala Ile Arg His Gly Lys Ile
1 5 10 15

Thr Thr Glu Ala Leu Arg Glu Arg Pro Ala Tyr Pro Thr Trp Ala Met
20 25 30

Lys Leu Thr Met Ala Ile Thr Gly Leu Met Phe Gly Gly Phe Val Leu
35 40 45

Val His Met Ile Gly Asn Leu Lys Ile Phe Met Pro Asp Tyr Ala Ala

```
     50                  55                  60

Asp Ser Ala His Pro Gly Glu Ala Gln Val Asp Val Tyr Gly Glu Phe
 65                  70                  75                  80

Leu Arg Glu Ile Gly Ser Pro Ile Leu Pro
                 85                  90


<210> 2925
<211> 523
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(523)
<223> RXA02827

<400> 2925
cggtttactt ttatttatcg aatgaatcat gtacatagaa taataagcat taaaggggg 60

gcgggtagga agaagcagcc gtgtcgcata tgcttacttt atg tat gag cag cag   115
                                              Met Tyr Glu Gln Gln
                                                1               5

aag atc ctt aac gaa gtc agt gaa aaa cgt ctt cag gca atc aaa gat   163
Lys Ile Leu Asn Glu Val Ser Glu Lys Arg Leu Gln Ala Ile Lys Asp
                10                  15                  20

ttt aca gaa ctg gga tct gga ttc aag att gcg atg cgg gat ctt tcc   211
Phe Thr Glu Leu Gly Ser Gly Phe Lys Ile Ala Met Arg Asp Leu Ser
            25                  30                  35

att cgc ggt gca ggt aat ctc tta ggt gct cag cag cat gga ttt att   259
Ile Arg Gly Ala Gly Asn Leu Leu Gly Ala Gln Gln His Gly Phe Ile
        40                  45                  50

gat gca gtc ggt ttc gat atg tat tct caa atg cta agc gaa gct gtt   307
Asp Ala Val Gly Phe Asp Met Tyr Ser Gln Met Leu Ser Glu Ala Val
    55                  60                  65

tnt cgt aaa caa gga aag aat agt caa gtg gag aag ncc nct gtt gag   355
Xaa Arg Lys Gln Gly Lys Asn Ser Gln Val Glu Lys Xaa Xaa Val Glu
70                  75                  80                  85

atc gac cnc ggt gtc gat gcg tat cta cct gaa aca tac gtg gca gat   403
Ile Asp Xaa Gly Val Asp Ala Tyr Leu Pro Glu Thr Tyr Val Ala Asp
                90                  95                 100

can cgg cag aaa atc gag atc tat aaa cga att cgt gaa ctt gat tcg   451
Xaa Arg Gln Lys Ile Glu Ile Tyr Lys Arg Ile Arg Glu Leu Asp Ser
            105                 110                 115

caa gaa atg cta gat gaa cta gaa gat gat ctg ctc gac cgt ttt gga   499
Gln Glu Met Leu Asp Glu Leu Glu Asp Asp Leu Leu Asp Arg Phe Gly
        120                 125                 130

gaa can cca gaa gaa gta gca cat                                  523
Glu Xaa Pro Glu Glu Val Ala His
    135                 140
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<210> 2926
<211> 141
<212> PRT
<213> Corynebacterium glutamicum

<400> 2926
Met Tyr Glu Gln Gln Lys Ile Leu Asn Glu Val Ser Glu Lys Arg Leu
1 5 10 15

Gln Ala Ile Lys Asp Phe Thr Glu Leu Gly Ser Gly Phe Lys Ile Ala
20 25 30

Met Arg Asp Leu Ser Ile Arg Gly Ala Gly Asn Leu Leu Gly Ala Gln
35 40 45

Gln His Gly Phe Ile Asp Ala Val Gly Phe Asp Met Tyr Ser Gln Met
50 55 60

Leu Ser Glu Ala Val Xaa Arg Lys Gln Gly Lys Asn Ser Gln Val Glu
65 70 75 80

Lys Xaa Xaa Val Glu Ile Asp Xaa Gly Val Asp Ala Tyr Leu Pro Glu
85 90 95

Thr Tyr Val Ala Asp Xaa Arg Gln Lys Ile Glu Ile Tyr Lys Arg Ile
100 105 110

Arg Glu Leu Asp Ser Gln Glu Met Leu Asp Glu Leu Glu Asp Asp Leu
115 120 125

Leu Asp Arg Phe Gly Glu Xaa Pro Glu Glu Val Ala His
130 135 140

<210> 2927
<211> 356
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(342)
<223> RXA02842

<400> 2927
gat gcg gga ttt gtg tac ttc ggt gaa atc gat gat gct ggc cat att 48
Asp Ala Gly Phe Val Tyr Phe Gly Glu Ile Asp Asp Ala Gly His Ile
1 5 10 15

ttc ggc ctg gca ggc gac gaa tac cga ggg ggg att cgc agg gtc gac 96
Phe Gly Leu Ala Gly Asp Glu Tyr Arg Gly Gly Ile Arg Arg Val Asp
20 25 30

acc cac gtg aag aaa gtt ctt tct gaa gtg tca cga cgc tcc gac gag 144
Thr His Val Lys Lys Val Leu Ser Glu Val Ser Arg Arg Ser Asp Glu
35 40 45

ctc ggg gag gac tgg ctg gta gtg atc aca act gat cat ggt cac ctt 192
Leu Gly Glu Asp Trp Leu Val Val Ile Thr Thr Asp His Gly His Leu

```
     50                  55                  60

gat gag ggc ggg cac ggc ggc acc acc gat cgg gag cga gaa tcc tgg   240
Asp Glu Gly Gly His Gly Gly Thr Thr Asp Arg Glu Arg Glu Ser Trp
 65                  70                  75                  80

atc atc acg tgg agc ccg cac cgg gaa ctg cca cag tgg cct gaa gaa   288
Ile Ile Thr Trp Ser Pro His Arg Glu Leu Pro Gln Trp Pro Glu Glu
                85                  90                  95

att gcg ccg cnt gag ctg gca gaa ctg atg ctt gtg gag cgc cga acc   336
Ile Ala Pro Xaa Glu Leu Ala Glu Leu Met Leu Val Glu Arg Arg Thr
            100                 105                 110

ttg agg tgattgtcac taaa                                          356
Leu Arg
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<210> 2928
<211> 114
<212> PRT
<213> Corynebacterium glutamicum

<400> 2928

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Asp Ala Gly Phe Val Tyr Phe Gly Glu Ile Asp Asp Ala Gly His Ile
  1               5                  10                  15

Phe Gly Leu Ala Gly Asp Glu Tyr Arg Gly Gly Ile Arg Arg Val Asp
             20                  25                  30

Thr His Val Lys Lys Val Leu Ser Glu Val Ser Arg Arg Ser Asp Glu
         35                  40                  45

Leu Gly Glu Asp Trp Leu Val Val Ile Thr Thr Asp His Gly His Leu
     50                  55                  60

Asp Glu Gly Gly His Gly Gly Thr Thr Asp Arg Glu Arg Glu Ser Trp
 65                  70                  75                  80

Ile Ile Thr Trp Ser Pro His Arg Glu Leu Pro Gln Trp Pro Glu Glu
                85                  90                  95

Ile Ala Pro Xaa Glu Leu Ala Glu Leu Met Leu Val Glu Arg Arg Thr
            100                 105                 110

Leu Arg
```

<210> 2929
<211> 615
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(615)
<223> RXA02845

<400> 2929

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gag gat cac acc tca atg ctc acc cac ttt tcc gca gct gtc ggc atg   48
Glu Asp His Thr Ser Met Leu Thr His Phe Ser Ala Ala Val Gly Met
  1               5                  10                  15

cat gac cgc gat ccg gct cgc ttc cca ggc cag ggc gac ggt tcc tac   96
His Asp Arg Asp Pro Ala Arg Phe Pro Gly Gln Gly Asp Gly Ser Tyr
            20                  25                  30

ccg gat ctt ttt tgg ctg tac aaa aac gcc ctc aac ctg gtc att agc   144
Pro Asp Leu Phe Trp Leu Tyr Lys Asn Ala Leu Asn Leu Val Ile Ser
        35                  40                  45

tca gtg ttg ttc acc cgt gag cag atg gac aac atg ctc gat cag atg   192
Ser Val Leu Phe Thr Arg Glu Gln Met Asp Asn Met Leu Asp Gln Met
    50                  55                  60

gat gaa cac ttc acg cgc gcg ggt atc ccg cgc atc gcg att aat att   240
Asp Glu His Phe Thr Arg Ala Gly Ile Pro Arg Ile Ala Ile Asn Ile
65                  70                  75                  80

gag cgc cgc gac gac gcc ctg atg aac ggc tcc ctc gag cgt gcg cta   288
Glu Arg Arg Asp Asp Ala Leu Met Asn Gly Ser Leu Glu Arg Ala Leu
                85                  90                  95

gag ctg caa gag ctt atc gac gcc tcc cag cac gac gat ccc ttc gac   336
Glu Leu Gln Glu Leu Ile Asp Ala Ser Gln His Asp Asp Pro Phe Asp
            100                 105                 110

gac tgc cca acc tgc caa att gca gga aaa gcg gca ctc gca atg gca   384
Asp Cys Pro Thr Cys Gln Ile Ala Gly Lys Ala Ala Leu Ala Met Ala
        115                 120                 125

gca gat gat tac gac gaa acc caa aac ctc gtc tcc caa atc atc agc   432
Ala Asp Asp Tyr Asp Glu Thr Gln Asn Leu Val Ser Gln Ile Ile Ser
    130                 135                 140

tac gga tcc atc ggc tgc gtc atg gaa cca gag acc acc ctc gct gcg   480
Tyr Gly Ser Ile Gly Cys Val Met Glu Pro Glu Thr Thr Leu Ala Ala
145                 150                 155                 160

ttc atg ctg cgt gtg ctt aag tcc ggc gat gct gat tat gcc cgc tac   528
Phe Met Leu Arg Val Leu Lys Ser Gly Asp Ala Asp Tyr Ala Arg Tyr
                165                 170                 175

ctg caa gat gtc agt gcg aag gca aac cca gaa ttc cag tcc ctt gat   576
Leu Gln Asp Val Ser Ala Lys Ala Asn Pro Glu Phe Gln Ser Leu Asp
            180                 185                 190

tcc gtt gga cgc cac cta gaa ttc ctc ggc atc act gga               615
Ser Val Gly Arg His Leu Glu Phe Leu Gly Ile Thr Gly
        195                 200                 205
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<210> 2930
<211> 205
<212> PRT
<213> Corynebacterium glutamicum

<400> 2930

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Glu Asp His Thr Ser Met Leu Thr His Phe Ser Ala Ala Val Gly Met
  1               5                  10                  15
```

```
His Asp Arg Asp Pro Ala Arg Phe Pro Gly Gln Gly Asp Gly Ser Tyr
            20                  25                  30

Pro Asp Leu Phe Trp Leu Tyr Lys Asn Ala Leu Asn Leu Val Ile Ser
        35                  40                  45

Ser Val Leu Phe Thr Arg Glu Gln Met Asp Asn Met Leu Asp Gln Met
    50                  55                  60

Asp Glu His Phe Thr Arg Ala Gly Ile Pro Arg Ile Ala Ile Asn Ile
65                  70                  75                  80

Glu Arg Arg Asp Asp Ala Leu Met Asn Gly Ser Leu Glu Arg Ala Leu
                85                  90                  95

Glu Leu Gln Glu Leu Ile Asp Ala Ser Gln His Asp Asp Pro Phe Asp
            100                 105                 110

Asp Cys Pro Thr Cys Gln Ile Ala Gly Lys Ala Ala Leu Ala Met Ala
        115                 120                 125

Ala Asp Asp Tyr Asp Glu Thr Gln Asn Leu Val Ser Gln Ile Ile Ser
    130                 135                 140

Tyr Gly Ser Ile Gly Cys Val Met Glu Pro Glu Thr Thr Leu Ala Ala
145                 150                 155                 160

Phe Met Leu Arg Val Leu Lys Ser Gly Asp Ala Asp Tyr Ala Arg Tyr
                165                 170                 175

Leu Gln Asp Val Ser Ala Lys Ala Asn Pro Glu Phe Gln Ser Leu Asp
            180                 185                 190

Ser Val Gly Arg His Leu Glu Phe Leu Gly Ile Thr Gly
        195                 200                 205


<210> 2931
<211> 499
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(499)
<223> RXA02848

<400> 2931
agcaaggacc gcaacaactg gggcaacctg gatgagcgtc tgtctcgccc gaacacgttt 60

aaccccagcg cgtttcagaa tgtgaatttc ttctagttac atg cag atc gtt ctg   115
                                                Met Gln Ile Val Leu
                                                  1               5

gct tcg cag tcc ccg tcc cgc cga aga atc ctc aat tcg gcg ggc gtc   163
Ala Ser Gln Ser Pro Ser Arg Arg Arg Ile Leu Asn Ser Ala Gly Val
                10                  15                  20

gag ccc ctc atc cac cca gct gat gtt gat gag gac gcg ctc ctt cac   211
Glu Pro Leu Ile His Pro Ala Asp Val Asp Glu Asp Ala Leu Leu His
```

```
            25                  30                  35

tcc ctc aac ggc tct gcg ccg gag gag atc gtc cgc cag ctt gcg ctg   259
Ser Leu Asn Gly Ser Ala Pro Glu Glu Ile Val Arg Gln Leu Ala Leu
        40                  45                  50

gct aaa gca cag gtg gtt gcg ccg tcc tat ccg ggc gac gtc gtc atc   307
Ala Lys Ala Gln Val Val Ala Pro Ser Tyr Pro Gly Asp Val Val Ile
    55                  60                  65

ggt ggc gat tcc atg ctg ctt atc gac gcc acc ctc caa ggc aag ccg   355
Gly Gly Asp Ser Met Leu Leu Ile Asp Ala Thr Leu Gln Gly Lys Pro
70                  75                  80                  85

cac acc cgc gaa gcc acc atc gaa aga tgg aaa caa caa cgc ggc aac   403
His Thr Arg Glu Ala Thr Ile Glu Arg Trp Lys Gln Gln Arg Gly Asn
                90                  95                  100

aag gcc aca ctg atc acc ggc cac gcc atc atc ttt ggc gat gaa gtg   451
Lys Ala Thr Leu Ile Thr Gly His Ala Ile Ile Phe Gly Asp Glu Val
            105                 110                 115

atc gtg gag tcc tcc tcc acc aac att cat ttc gcc gag gcc agc gat   499
Ile Val Glu Ser Ser Ser Thr Asn Ile His Phe Ala Glu Ala Ser Asp
        120                 125                 130


<210> 2932
<211> 133
<212> PRT
<213> Corynebacterium glutamicum

<400> 2932
Met Gln Ile Val Leu Ala Ser Gln Ser Pro Ser Arg Arg Arg Ile Leu
  1               5                  10                  15

Asn Ser Ala Gly Val Glu Pro Leu Ile His Pro Ala Asp Val Asp Glu
             20                  25                  30

Asp Ala Leu Leu His Ser Leu Asn Gly Ser Ala Pro Glu Glu Ile Val
         35                  40                  45

Arg Gln Leu Ala Leu Ala Lys Ala Gln Val Val Ala Pro Ser Tyr Pro
     50                  55                  60

Gly Asp Val Val Ile Gly Gly Asp Ser Met Leu Leu Ile Asp Ala Thr
 65                  70                  75                  80

Leu Gln Gly Lys Pro His Thr Arg Glu Ala Thr Ile Glu Arg Trp Lys
                 85                  90                  95

Gln Gln Arg Gly Asn Lys Ala Thr Leu Ile Thr Gly His Ala Ile Ile
            100                 105                 110

Phe Gly Asp Glu Val Ile Val Glu Ser Ser Ser Thr Asn Ile His Phe
        115                 120                 125

Ala Glu Ala Ser Asp
    130
```